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NDRERVNEAREELTRML 111

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RESULT 15

CAL2_P,
AC 094715
DT 28-FEB
DT 28-F
В
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                                                                                                                                   Query Match
Best Local :
                                                                                                            Matches
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Q94715;
28-FEB-2003
28-FEB-2003
28-FEB-2003
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ACT_SITE
DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00640; THIOL_PROTEASE_ASN; PROSITE; PS00139; THIOL_PROTEASE_CYS; PROSITE; PS00639; THIOL_PROTEASE_HIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96248439; PubMed-8665938;
Voelkel H., Kurz U., Linder J., Klumpp S., Gnau V., Jung G.,
Schultz J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative cathepsin L2 (EC 3.4.22.15) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00705; PAPAIN.
ProDom; PD000158; Peptidase_C1; 1.
SMART; SM00645; Pept_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X91756; CAA62871.1;
PIR; S68784; S68784.
HSSP; O60911; 1FHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cathepsin L is an intracellular and extracellular protease in Paramecium tetraurella: Purification, cloning, sequencing and specific inhibition by its expressed propeptide.";
Eur. J. Blochem. 238:198-206(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paramecium tetraurelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: May be involved in extracellular digestion.
CATALYTIC ACTIVITY: Specificity close to that of papain. As compared to cathepsin B, cathepsin L exhibits higher activity towards protein substrates, but has little activity on Z-Arg-Arg-NHMec, and no peptidyl-dipeptidase activity.
SUBCELULIAR ICCATION: Secreted.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CAUTION: This protein may be non-functional as it lacks the cysteine active site residue which is replaced by Gly-118.
40 SNKRMIEEHNQR
                                                                                                          Similarity
8; Conserv
                                                   SNKTRIDEANQR 12
                                                                                                                                                                                                                    118
247
264
115
240
294 AA;
                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protease.
                                                                                                                                                                                                                      33627
                                                                                                                                45.8%;
                                                                                                                                                                                                                      MW.
                                                                                                                                                                                                                                        ACTIVATION PEPTIDE.
PUTATIVE CATHEPSIN L2.
POSITION OF ACTIVE SITE CYS.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                              Score 38; DB
Pred. No. 29;
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                                                                                                                                                                                                                    6FD686A0176BEC51 CRC64;
                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FALSE_NEG.
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                                                                                                                                                             DB 1;
                                                                                                       ω,
                                                                                                                                                             Length 294;
                                                                                                       Indels
                                                                                                       0;
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Search completed: September 16, Job time: 4.42857 secs

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RESULT 14
ARR2_MOUSE
ID ARR2_AC P1650
DT 01-AU
DT 01-AU
DT 15-DE
DE ADP-I
GN ARR2_.
OS Mus n
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Best Local
                                                                                                                                                                                     P16500; P10947;
01-UUL-1989 (Rel. 11, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPECIES-Bovine;
MEDLINE-88289746;
Price S.R., Nightingale M., Tsai S.-C.,
Chen H.-C., Moss J., Vaughan M.;
"Guanine nucleotide-binding proteins the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P., Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J., Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L., Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.; "Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti psynA megaplasmid."; Proc. Natl. Acad. Sci. U.S.A. 98.9883-9888(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ225896; CAB38102.1; ALT_FRAME. EMBL; AE007273; AAK65521.1; -. PIR; G95369; G95369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=1021;
MEDLINE=21396509; PubMed=11481432;
                                                                                                                              Eukaryota; Metazoa; Chordata;
                                                                                                                                                                       Mus musculus (Mouse),
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                    NCBI_TaxID=10090,
                                                                                                                                            Bos taurus
                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                     ARF2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endoglycanase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           symbiotic effectiveness
                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nodulation; Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002514; Transposase_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The eff-482 locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Becker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sharypova L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: REF.1 SEQUENCE DIFFERS FROM FRAMESHIFTS IN POSITION 124 AND 137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEGATIVELY AUTOREGULATED.
SIMILARITY: BELONGS TO THE SYRB FAMILY
                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF01527; Transposase_
                                                                                                                                                         norvegicus (Rat),
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                      RLEEENQRLRKLL 133
                                                                                                                                                                                                                                                                                                                                                                 RIDEANORATKML 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Swiss Institute of
                                                                                                                    Eutheria;
                                                                                                                                            (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us of Sinorhizobium meliloti CXM1-105 that influences iveness consists of three genes encoding an transcriptional regulator and an adenylate cyclase.
                                                                                                   a; Rodentia;
10116, 9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
17028
                                                                                                                                                                                                                                                                                                                                                                                                         45.8%;
53.8%;
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                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulation; Repressor; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB
Pred. No. 14;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            ω
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                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> H (IN REF. 1).
215627A0FAD4EBA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics
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       that enhance choleragen ADP
                                                                                                                                                                                                                                                                     181
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14;
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                                  Williamson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHOWN
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64
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                                K.C.,
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                                  Adamik R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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                                                                                                                              GTP-binding; Multigene family; Protein transport; Golgi stack NP_BIND 24 31 GTP (BY SIMILARITY). NP_BIND 67 129 GTP (BY SIMILARITY).
                                                                                                                                                                                                                              TIGREAMS; TIGRO0231; small_GTP; PROSITE; PS01019; ARF; 1.
                                                                                                                                                                                                                                                                                                            Pfam; PF00025; arf; 1.
PRINTS; PR00449; RASTRNSFRMNG.
PRINTS; PR00328; SAR1GTPBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-Mouse; STF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=Rat; TISSUE=Brain;
Nightingale M.S., Price S.R.,
Submitted (XXX-1994) to the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmentally regulated, selectively expressed member of the ARF family of approximately 20-kDa guanine nucleotide-binding proteins.", J. Biol. Chem. 268:4863-4872(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=Bovine; TISSUE=Retina; MEDLINE=93186792; PubMed=8444865; Serventi I.M., Cavanaugh E., Moss J., Vaughan M.; Serventi I.M., Cavanaugh E., Moss J., Vaughan M.; "Characterization of the gene for ADP-ribosylation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribosyltransferase activity: nucleotide and deduced sequence of an ADP-ribosylation factor cDNA."; proc. Natl. Acad. Sci. U.S.A. 85:5488-5491(1988).
                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                 SMART; SM00177; ARF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
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                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005225;
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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J. Biochem. 120:813-819(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure and intracellular localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hosaka M., Toda K., Takatsu H.,
                                                                                                                                                                                                                                                                                                                                                    k; JC4946; JC4946; JC4946; JC4946; JC4946; JC59; P32889; HUR.
Sp; P32889; HUR.
Sp; P32889; Arf2; JRF2959; JRF2959; JRF2958; ARF25AR.
InterPro; IPR0016689; ARF25AR.
IPR001806; Ras_trnsfrmng.
IPR001806; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: GTP-BINDING PROTEIN THAT FUNCTIONS AS AN ALLOSTERIC ACTIVATOR OF THE CHOLERA TOXIN CATALYTIC SUBUNIT, AN ADPRIBATION OF THE CHOLERA TOXIN CATALYTIC SUBUNIT, AN ADPARAMSFERASE. INVOLVED IN PROTEIN TRAFFICKING; MAY MODULATE VESICLE BUDDING AND UNCOATING WITHIN THE GOLGI APPARATUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE ARF FAMILY OF GTP-BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A45422; A45422.
JC4946; JC4946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D87899; BAA13491.1;
Similarity 6; Conser
                                                                                                        181
  Conservative
                                                                                                     ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ICR;
                          45.8%;
35.3%;
                                                                                                     20746 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Tsuchiya M., Moss
EMBL/GenBank/DDBJ da
                          Pred.
                                                Score 38;
                                                                                                        95BE17A962B83016
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  Mismatches
                          NO.
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                                                  DB 1;
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of mouse F
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  4;
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                                                  Length 181;
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  Indels
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RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;
                                                                           Query Match
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Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. [4]
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"The DNA sequence of human chromosome 22.";
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Tilahun Y., Wright
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CAUTION: Ref.2
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AC004542; AAC12954.1;
BC019257; AAH19257.1;
AL133637; CAB63760.1;
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459161807B8B53F6 CRC64;
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01-FEB-1995
28-FEB-2003
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Wohldman P
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Connell M., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                     Probable transcriptional regulator syrB2.

SYRB2 OR RA0863 OR SMA1586.

Rhizobium meliloti (Sinorhizobium meliloti).

Plasmid pSymA (megaplasmid 1).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.

RCBI_TaxID-382;
                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Probable transcriptional regulator syrB2.
                                                                                                                                                                                                             SYB2_RHIME Q9Z3Q1;
                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 9:
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MEDLINE-99413305;
           SEQUENCE FROM
STRAIN-CXM1-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WormPep;
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elegans.";
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                                                                                                                                                                                                                                                                                                           368 SNKTDNYALDEANQSA 383
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918 AA; 9
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1 protein F59B2.12 in chron
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PubMed=10485295
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62.58;
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Pred. No. 82;
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GO; GO:0006916; P:anti-apoptosis; IDA.
InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 2.
Pfam; PF00057; Zf-C3HC4; 1.
SMART; SM00238; BIR; 2.
SMART; SM00238; BIR; 2.
                                                                                                                                                                                                                                                                                                          EMBL; 149440; AAC41609.1; -
PDB; 1JD4; 05-DEC-01.
PDB; 1JD5; 05-DEC-01.
PDB; 1JD5; 05-DEC-01.
FlyBase; FBgn0003691; th.
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ProDom; PD004104; Nop
mRNA processing; mRNA
CONFLICT 361 39
                                  PROSITE; PS01282; BIR_REPEAT_1; 2.

PROSITE; PS50143; BIR_REPEAT_2; 2.

PROSITE; PS00518; ZF_RING_1; FALSE_NEG.

PROSITE; PS50089; ZF_RING_2; 1.
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MEDLINE-96128128; Pu
Hay B.A., Wassarman
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Hay B.A., Wassarman D.A., Rubin G.M.;
"Drosophila homologs of baculovirus inhibitor
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IAP1 OR TH
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01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAP1_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 83:1253-1262(1995).

FUNCTION: APPOPTOTIC SUPPRESSOR. OVEREXPRESSION
HID-DEPENDENT CELL DEATH IN THE EYE.

SIMILARITY: BELONGS TO THE IAP FAMILY.
SIMILARITY: Contains 2 BIR repeats.
SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTRIDEANQRATKML
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Zinc-finger; Repeat; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
394
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42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      license agreement
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4 TNPKRKELGENLGSTRKNSDYRMSDNYKIGWNLA
DQPKKKRAGRKFRKYKEKFRLSHYRQLQNRMEFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
(Inhibitor of apoptosis 1) (dIAP1) (Thread
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Pred.
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; 1C320B8630EEF5C8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438
                                                                                                                                                                                                                                                                                     activity; IDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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ACD DITION OF THE PROPERTY OF 
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SQ
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RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Clegg S.M., Coble V.E., Cole C.G., Collier R.E., Connor R.,
Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Clegg S.M., Coby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Clegg S.M., Cokree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Hill R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
Hunt S.E., Jones M.C., Kershaw J., Kinberley A.M., King A.,
RA Haird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA McClay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T.,
RA McClay J., Wolaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Odell C.N., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilning L.,
RA Wildhi C.L., Hubbard T., Bantley D. R., Rock S., Rogers I., Shiffith N. M.
RA Wildhi C.L., Hubbard T., Bantley D. R., Rock S., Rogers I., Shiffith N. M.
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Best Local
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                                                                                Wright C.L., Hubbard T., Bentley D.R., Beck S., Røgers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shintani A., Shibuya K., Voshizaki Y., Aoki N., Mitsuyama S., Shintani A., Shibuya K., Voshizaki Y., Aoki N., Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L., Wang O., Wang Z., White J., Milligham D., Wu H., Yao Z., Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Tulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Lindowski M., Lindowski B., Goela D., Graves T., Hawkins J., Lindowski B., Goela D., Graves T., Hawkins J., Lindowski B., Lindowski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Y6X9; Q9UF28; Q9Y6V2;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
ZN_FING
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=20057165; PubMed=10591208;
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                                                      Kemp K., Latreille P., Layman
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391
438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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Primates;
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ky P., Rohlfing
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Best Local S
Matches
Dietrich F.S., Mulligan J.T., He Araujo R., Aviles E., Berno A., Cherry J.M., Chung E., Duncan M. Hunicke-Smith S., Hyman R.W., K. Lin D., Mosedale D., Nakahara K. Oh C., Petel F.X., Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 ()
01-FEB-1995 ()
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Saccharomycetales;
NCBI_TaxID-4932;
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Nature 406:959-964(2000).
-i- SUBCELLULAR LOCATION: Attached
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Bridy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                              PubMed=9169868;
                                                                                                                                                                                                                   STRAIN-S288c
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P40038;
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-
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L; M25761; AAA25880.1; -.
L; X58714; CAA41550.1; -.
L; A07695; CAA00707.1; -.
L; AE004712; AAG06241.1; -.
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Hennessy K.M., Yelton M.A., Allen E.,
. Brennan T., Carpenter J., Chen E.,
M., Guzman E., Hartzell G.,
Kayser A., Komp C., Lashkari D., Lew H.,
K., Namath A., Norgren R., Oefner P.,
Sehl P., Schramm S., Shogren T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             in PET117-CEM1
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, Yuan Y.,
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PR31_YEAST
ID PR31_Y
AC P49704
DT 01-OCT
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OC Sacche
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DR EMBL;
DR EMBL;
DR SGD;
DR GG;
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between
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SGD;
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                                                                                                                                      the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is it modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeas Eukaryota; Fungi; Ascomycota; Saccharosaccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pre-mRNA splicing factor PRP31.
PRP31 OR YGR091W.
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(၀၀)
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                                                                                                EMBL; U31970; EMBL; Z72876;
                                                                                                                                                                                                                                                                                                                                             "The PRP31 gene encodes a novel protein splicing in Saccharomyces cerevisiae."; Nucleic Acids Res. 24:1164-1170(1996).
                                                                                                                                                                                                                                                                                    Wedler H., Scharfe M.,
Submitted (MAY-1996) t
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96184869; PubMed=8604353;
Weidenhammer E.M., Singh M., Ruiz-Noriega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P49704;
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R; $64386.
R; $64386.
Sp; $6003323; PRP31.
D; $00003323; C:small nuclear ribonu O; GO:0008248; F:pre-mRNA splicing for GO:0006371; P:mRNA splicing; IPI.
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                                                                                                                                                                                                                                                        FUNCTION: REQUIRED FOR PRE-MRNA SPLICING. SUBCELLULAR LOCATION: Nuclear (Potential).
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CAA97094.1;
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                                                      nuclear ribonucleoprotein
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                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
PRE-MRNA SPLICING.
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cetaceae; Saccharomyces
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catabolism; I
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01-JUN-1994
01-JUN-1994
15-SEP-2003
between the the European
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                    MEDLINE=97417485; PubMed=9272858;
MEDLINE=97417485; PubMed=9272858;
Risinger C., Deitcher D.L., Lundell I.,
"Complex gene organization of synaptic melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                   SNAPZD.

Drosophila melanogaster (Fruit 11y).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Eukaryota; Endopterygota; Diptera; Brachycera;

Neoptera; Endopterygota; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005803; C:secretory vesicle; TAS.
GO: GO:0005402; F:vesicle targeting; TAS.
GO; GO:0006944; P:membrane fusion; TAS.
GO; GO:0006903; P:non-selective vesicle targeting;
GO; GO:0006892; P:post Golgi transport; TAS.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000928; SNAP-25.
                                                                                                                                                        Gene
                                                                                                                                                                                                                                              Risinger C., Blomqvist A.G., Lundell I., Lambertsson A., Nassel D., Pieribone V.A., Brodin L., Larhammar D.; "Evolutionary conservation of synaptosome-associated protein (SNAP-25) shown by Drosophila and Torpedo cDNA clones."; J. Biol. Chem. 268:24408-24414(1993).
                                                                               <del>-</del>
                                                                                                                                                                                                                                                                                                             MEDLINE=94043281; PubMed=8226991;
                                                                                                                                                                                                                                                                                                                           TISSUE=Head
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Synaptosomal-associated
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SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
Protein transport; Synaptoson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                               e 194:169-177(1997).

FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED VESICLE DOCKING AND MEMBRANE FUSION.

SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS THE NERVE TERMINAL.

TISSUE SPECIFICITY: EXCLUSIVELY FOUND IN BRAIN AND GANGLIA. SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.

SIMILARITY: Contains 2 t-SNAPE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193
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9; Conserv
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208
89
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T-SNARE COILED-COIL HOMOLOGY 2.
R >> S (in isoform SNAP-23b).
/FTId=VSP_006187.
Missing (in isoform SNAP-23b).
/FTId=VSP_006188.
A -> V (IN REF. 1).
W; AC378E9786C3A239 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
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era; Muscomorpha;
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EMBL; U81153; AAB39757.1; JOINED.
EMBL; U81147; AAB39757.1; JOINED.
EMBL; U81148; AAB39757.1; JOINED.
EMBL; U81149; AAB39757.1; JOINED.
EMBL; U81150; AAB39757.1; JOINED.
EMBL; U81151; AAB39757.1; JOINED.
EMBL; U81152; AAB39757.1; JOINED.
                                                                   "Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecul cloning, sequence, and expression in Escherichia coli.";

J. Bacteriol. 171:4130-4137(1989).
SEQUENCE FROM N.A STRAIN=ATCC 15692 MEDLINE=92268853;
                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=89327122; PubMed=2502533;
Duchene M., Barron C., Schweizer A.,
                                                                                                                                                                                                                           Cornelis P., Bouia A., Belarbi A., Guyor Hannaert V., Hubert J.-C.; "Cloning and analysis of the gene for the poprotein from Pseudomonas aeruginosa. Mol. Microbiol. 3:421-428(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Major outer membrane lipoprotein precursor (M
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SEQUENCE
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MEDLINE=89313294; PubMed=2473376;
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Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
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P11221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Lipoprotein I).
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212
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26 88 T-SNARE COILED-COIL
148 210 T-SNARE COILED-COIL
91 99 CYS-RICH.
(12 AA; 23685 MW; BDC90649AlAF3AC8 C
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30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Risinger C., Blomqvist A.G., Lundell I., Lambertsson / Massel D., Pieribone V.A., Brodin L., Larhammar D.; "Evolutionary conservation of synaptosome-associated [SNAP-25] shown by Drosophila and Torpedo cDNA clones (SNAP-25) shown by Drosophila and Torpedo cDNA clones (JBAOL. Chem. 268:24408-24414(1993)).
                                                        Ravichandran V., Chawla A., Roche P.A.;
"Identification of a novel syntaxin- and syntrotein SNAP-23, expressed in non-neuronal J. Biol. Chem. 271:13300-13303(1996).
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SN23_HUMAN (
O00161; O00162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
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   SEQUENCE
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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MEDLINE-94043281; PubMed-8226991;
                                                                                                                                                                                     MEDLINE=96278745; PubMed=8663154;
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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IPR000727; T_SNARE
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(Rel. 39, Last sequence update)
(Rel. 42, Last annotation updat
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T-SNARE COILED-COIL HOMOLOGY
T-SNARE COILED-COIL HOMOLOGY
CYS-RICH.
; 58FE471A9234B8B1 CRC64;
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SNAP-23A
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Catarrhini;
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nal tissues.";
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EMBL; EMBL; PIR; PIR;

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AJ011915; CAA09864.1; -. BC000148; AAH00148.1; -. BC003686; AAH03686.1; -. BC022890; AAH22890.1; -.

Genew;

HGNC:11131;

SNAP23

602534;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Salska U., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Neutrophils;
MEDLINE=97224437; PubMed=9070898;
Mollinedo F., Lazo P.A.;
"Identification of two isoforms of the vesicle-membrane "Identification of two isoforms of the vesicle-membrane SNAP-23 in human neutrophils and HL-60 cells.";
SNAP-23 in human neutrophils and HL-60 cells.";
                                                                                                                                                                                                                                                                                                     This SWI
between
EMBL;
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                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alternative splicing."
Submitted (OCT-1998) to
                                                                                                                                                  or send an
                                                                                                                                                                              entities requires a
                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-22388257;
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=SNAP-23b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=SNAP-23a;
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                               Y09568; CAA70761.1;
                                                                                       U55936; AAC50537.1;
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                                                                                                                                                  email to license@isb-sib.ch).
                                                        CAA70760.1;
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and chromosomal localization of h
23 (SNAP-23) gene and generation
                                                                                                                                                                              license agreement
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Jensen

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REPUBLICAN CONTRACTOR 
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RX MEDLINE=22388557; PubMed=12477932;

RX MEDLINE=22388557; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Walkernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butkersley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkersley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkersley R.W., Touchman J.W., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

RT "man and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catsicas
Wilson M.
                  "The 25 kDa synaptosomal-associated protein SNAP-25 is the methionine-rich polypeptide in rapid axonal transport and substrate for palmitoylation in adult CNS.";
J. Neurosci. 12:4634-4641(1992).
                                                                                                                                                                                                                                                                                                                                                               SPECIES=Chicken;
MEDLINE=93389738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The identification of a novel synaptosomal-associated SNAP-25, differentially expressed by neuronal subpopulations. Cell Biol. 109:3039-3052(1989).
                                                                                                                                                       MEDLINE=93100552;
                                                                                                                                                                                                          PALMITOYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES-Chicken; TISSUE-Retina;
MEDLINE-91126080; PubMed-1992470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cho
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MEDLINE=90078337; PubMed=2592413;
Oyler G.A., Higgins G.A., Hart R.A.,
Bloom F.E., Wilson M.C.;
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25 kDa synant
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                                                                                                                                                                                                                                                     e chicken gene for t isoforms of the r 3:67-76(1993).
                                                                                                                            PubMed=1281490;
T.M., Wilson M.
                                                                                                                                                                                                                                                                                                                                                                 PubMed-8377193;
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U.S.A. 88:785-789(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D., Blomqvist A.,
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EMBL/GenBank/DDBJ
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Best Local :
                                                      SN25_TORMA
P36976;
01-JUN-1994
01-JUN-1994
15-SEP-2003
                                                                                                                               _TORMA
           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-Sep-2003 (Rel. 42, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25).
Torpedo marmorata (Marbled electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit modified and this st entities requires a
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                                                                                                                                                                                                                                                                                                                 EMBL;
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Brain Res. Mol. Brain Res. 37:49-62(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Rat;
MEDLINE-96346613; PubMed-8738135;
Medline-96346613; PubMed-8738135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobsson G., Piehl F., Bark I.C., Zha "Differential subcellular localization"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION OF SPECIES=Rat;
                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: tSNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates proteins involved in vesicle docking and membrane fusion. SUBUNIT: Binds to syntaxin-1.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                       L; L19761; AAC37546.1; -.
L; L19760; AAC37545.1; -.
L; D121267; BAAD2370.1; -.
L; AL023913; CAB42860.1; -.
L; AL023913; CAC34534.1; -.
L; AL023913; CAC34534.1; -.
L; M2012; AAA61741.1; -.
L; M2012; AAA61741.1; -.
L; M2012; AAA61741.1; -.
L; M2012; AAA61741.1; -.
L; M2012; AAA61761.1; -.
L; AB003991; BAA20151.1; -.
L; AB003991; BAA20151.1; -.
L; AB003992; BAA20151.1; -.
L; AB003992; BAA20151.1; -.
L; AB003992; BAA20151.1; -.
L; AB003992; BAA2015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note-Has been shown to exist only in human and rat so far; TISSUE SPECIFICITY: NEURONS OF THE NEOCORTEX, HIPPOCAMPUS, PIRIFORM CORPEX, ANTERIOR THALAMIC NUCLEI, PONTINE NUCLEI, A GRANULE CELLS OF THE CEREBELLUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms=2; Comment=Isoforms differ by the usage of two homologous exons (5a and 5b) which encode for and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PALMITOYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=SNAP-25a; IsoId=P13795-2; Sequence=VSP_006186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=SNAP-25b;
                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                   L09253;
L09254;
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                                                                                                                                                                                                                                            17; Conserv
                                                                                                                                                                                       SNKTRIDEANQRATKML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                   AAA49070.1; -.
AAA49070.1; JOINED
                                                                                                                 STANDARD;
  Squalea;
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 Hypnosqualea; Pristiorajea;
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Pred. No. 2.9e-07;
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or positions
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  Batoidea;
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ID SNANACA CARAU
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Matches 17
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Best L
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PIR; I50480; I50480.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
 SN25_HUMAN
P13795; P3
                                                                                                                                                                                                           Synaptosome; Neuronē; Repeat; Coiled coil; Multigene family.
DOMAIN

19
81
T-SNARE COILED-COIL HOMOLOGY 1.
DOMAIN
138
200
T-SNARE COILED-COIL HOMOLOGY 2.
SEQUENCE
204 AA; 22843 MW; 458BBECFCFC09189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carassius auratus (Goldfish).
Eukaryota, Metazoa; Chordata;
Actinopterygii, Neopterygii; ?
Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Synaptosomal-associated protein 25A (SNAP-25A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SN2A_CARAU P36977;
                                                                                                                                                                                                                                                                                       SMART; SM00397; t_SNARE; 2. PROSITE; PS50192; T_SNARE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          goldfish.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS VESICLE DOCKING AND MEMBRANE FUSION. SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. Natl. Acad. Sci. U.S.A. 90:105
FUNCTION: MAY PLAY AN IMPORTANT
SPECIFIC NEURONAL SYSTEMS. ASSOC
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17; Conserv
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               STANDARD;
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92
22843
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t-SNARE coiled-coil homology domains.
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Teleostei;
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Pred. No.
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Pred.
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ORTANT ROLE IN THE SYNAPTIC FUNCTION
               PRT;
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Chapman J.C., Coville G.J., Deadman R., Dhami P.D., Dunn M.R.,

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.R.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Hammond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Lioyd D.M., Lovell J.D.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Ce C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Whitehead S.L., Whittaker P., Willey D.L., Walliams D.W., Thorpe A.,

RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Rocers T., Walliams S.A.,

RA Wilming L., Wary P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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01-FEB-1991
15-SEP-2003
   SEQUENCE E
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MEDLINE-96332494; PubMed-8760387;

Jagadish M.N., Fernandez C.S., Hewl

Gough K.H., Grusovin J., Verkuylen

Frenkel M.J., Ward C.W.;
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Gallus (Chicken).

Gallus (Chicken).

Eukaryota; Metazoa; Chordata;

Mammalia; Eutheria; Primates;

NCBI TaxID=9606, 9544, 10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbege A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
                                                                  Nature
[5]
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terminal protein SNAP-25.
Gene 139:291-292(1994)
[2]
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MEDLINE=94156217; PubMed=81:
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414:865-871(2001)
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                                 FROM
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116538.1; 81. SNAP-25.28; SNAP-25.27; T_SNARE 127.5; 1. SNARE: 2. T_SNARE; 2. T_SNARE	-!- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY!- SIMILARITY: Contains 2 t-SNARE coiled-coil home. This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are use by non-profit institutions as long as its modified and this statement is not removed. Usage entities requires a license agreement (See http://oor send an email to license@isb-sib.ch).	CO. NALL. ACED. SCI. U.S.A. 90:10598- FUNCTION: MAY PLAY AN IMPORTANT ROL. SPECIFIC NEURONAL SYSTEMS. ASSOCIATI VESICLE DOCKING AND MEMBRANE FUSION SUBCELLULAR LOCATION: COMPLEXED WITH THE MERVE TERMINAL. TISSUE SPECIFICITY: NEURONS OF THE PIRIFORM CORTEX, ANTERIOR THALAMIC GRANULE CELLS OF THE CEREBELLUM.	PubMed=8 mmar D.; synapse	ted poldfi	RD; Cre		4473 1 4473 1 504 1 558 1 693 1 770 1 829 1 887 1 952 1
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DR EMBL; U64862; AAM69078.1; -

DR WOrmPep; ZC8 4a; CE31264.

DR InterPro; IPR000533; Tropomyosin.

DR PRINTS; PR00194; TROPOMYOSIN.

KW Hypothetical protein.

SQ SEQUENCE 2396 AA; 273873 MW; 7A184CD36D9EE3DC CRC64;

Query Match

Best Local Similarity 60.0%; Pred. No. 81;

Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 KTRIDEANQRATKML 17

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Search completed: September 16, 2003, 19:29:42

Job time: 11.8182 secs
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Sibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                   Q95ZK3;
01-DEC-2001
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  Hypothetical
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EMBL: AKO17311: BAB30686.1; -.
MGD; MGI:109356; Snap23.
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STRAIN-C57BL/6J; TISSUE-Head;
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SEQUENCE
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MEDLINE-99069613; PubMed-9851916;
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01-MAR-2003
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Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                     STRAIN-Bristol
                                                                                                                  The sequence
                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                     "Genome sequence of the nematode C. investigating biology. The C. elegan Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
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STRAIN-Bristol N2;
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of C. elegan
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to the
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el. 22,
el. 23,
ZC8.4a.
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cda; Chromadorea; Caenorhabditis.

Rhabditida; Rhabditoidea;

Last sequence update)
Last annotation updat

Created)

PRT;

2396

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EMBL/GenBank/DDBJ cosmid ZC8.";

databases

ode C. elegans: a platform for elegans Sequencing Consortium.";

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"Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; U64862; ANK67253.1; -.
WormPep; 2C8.4b; CE28169.
                                                                                                                                                                                                                                                                                         Latreille P., Bradshaw H.; "The sequence of C. elegan Submitted (JUL-1996) to the
                                                                                                                                    InterPro; IPR005613; AIP3.
InterPro; IPR000533; Tropomyosin
Pfam; PF03915; AIP3; 1.
                                                                                                                                                                                                                                                                                                                                                                            pating biology. The C 282:2012-2018(1998).
KTRIDELNRRVENLL 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peloderinae;
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) to the
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                                                                              Length 2315;
                                                                                                                                                                                                                                                                                                                                                                                            Consortium.";
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RESULT 12
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ID 00904
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070377;
01-AUG-1998
01-AUG-1998
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997
01-OCT-2002
SNAP-25 homo
                                                                                                                                                 SMART; S
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bruns D., Engers S., Yang C., Ossig R., Jeromin A., Jahn R.;
"Inhibition of transmitter release correlates with the proteolytic activity of tetanus toxin and bottulinus toxin A in individual cultu synapses of Hirudo medicinalis.";
J. Neurosci. 17:1898-1910(1997).
EMBL; U85806; AAC47499.1;
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida. Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo NCBI_TaxID=6421;
009044
                                                                                                                                                                       InterPro; IPR000928; SNAP-25.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam: pF00025. FFFF or
                                                                                                                                                                                                 Biochem. J. 338:709-715(1999).
EMBL; AF052596; AAC06031.1; -.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=99162237; Pubmed=10051443;
St-Denis J.F., Cabaniols J.P., Cus
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                         SNAP-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSSITE; PS50192; T_SNARE; 2.
SEQUENCE 212 AA; 23802 MW;
                                                                                                                                                                                                EMBL; AF052596;
                                                                                                                                                                                                                       cells.";
                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                 SNAP-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "ILSSUE=Nerve cord;
MEDLINE=97197869;
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                                                                                                                                                                                                                                "SNAP-23 participates in SNARE
                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116
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                                                    192
                                                                                                                                   PF00835; SNAP-25; 1.
; SM00397; t_SNARE; 2.
;TE; PS50192; T_SNARE; 2.
;NCE 210 AA; 23235 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                194
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                                                                                             10;
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                                                                SNKTRIDEANQRATKML 17
                                                  THKNRIDIANTRAKKLI 208
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                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                               Chordata;
Rođentia;
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58.8%;
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58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                            PRT;
PRT;
                                                                                                                                                                                                                                Cushman S.W., Roche P.A.; complex assembly in rat adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8FF591DF32A4FCB6 CRC64;
                                                                                                                                    OD63E3A6F9FE3BA2 CRC64;
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annotation update)
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kiehi P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Lewis S., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.;
   MGD; MGI:109356; Snap23.
InterPro; IPR000928; SNAP-25.
InterPro; IPR0009727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; T_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 210 AA; 23261 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNAP23 OR SNUJ.
SNAP23 OR SNUJ.
Mus musculus (Mouse).
Metazoa; Chordata;
hervota; Metazoa; Rodentia;
                                                                                                   EMBL;
EMBL;
MGD;
                                                                                                                                                 EMBL;
EMBL;
                                                                                                                                                                                                  EMBL;
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Niki T., Okazawa H., Kubota T., Kasuga M.;
"Inhibition of the binding of SNAp-23 to Biochem. Biophys. Res. Commun. 234:257-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNDET (SNAP-23) (Synaptosomal-associated SNAP23 OR SNDT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         009044;
01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Syndet is a novel SNAP-25 related
tissues.";
                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                               "Functional annotation of a fu. 
Nature 409:685-690(2001). 
EMBL; AB000822; BAA20345-1; -. 
EMBL; U73143; AAB53597-1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129/SVJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97220227; PubMed=9067602; Wang G., Witkin J.W., Hao G., Ban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fat;
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[1]
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                                                                                                           L; AB000822; BAA20345.1; -...
L; U73143; AAB53597.1; -...
L; AF213257; AAF23503.1; JOINED.
L; AF213252; AAF23503.1; JOINED.
L; AF213252; AAF23503.1; JOINED.
L; AF213254; AAF23503.1; JOINED.
L; AF213254; AAF23503.1; JOINED.
L; AF213256; AAF23503.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    han V.V., Roche P.A.; e and chromosomal localization of the mouse SNAP-23 (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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04, Last sequence update)
22, Last annotation update
                                                                                                                                                                                                                                                                                                  full-length mouse cDNA collection.";
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Sciurognathi;
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   6919E127E16BA2C9 CRC64;
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i protein, i
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RESULT
Q8T3S4
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DT 01
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QRAXMI
ID QBAX
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DT Q1-M
DT Q1-M
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DC SNAP
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                          Q8T3S4 PRELIMINARY;
Q8T3S4;
Q8T3S4;
Q1-JUN-2002 (TrEMBLrel. 21, C
Q1-JUN-2002 (TrEMBLrel. 21, L
Q1-QCT-2002 (TrEMBLrel. 22, L
SNAP25 fusion protein.
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SEQUENCE FROM N.A.

KOLK S.M., Groffen A.J.A., Tuinhof R., Vernaye
Kolk S.M., Groffen A.J.A., Tuinhof R., Vernaye
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ
EMBL; AF335586; AAO13788.1; -
206 AA; 23122 MW; 2D1D0FD35E0C1DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8AXM2;
Q8AXM2;
01-MAR-2003
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01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOlk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roub Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF335587; AA013789.1; -
SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
     Loligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNAP25a.
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     pealeii
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14; Conser
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                                                                                                                                                                                                                                                                                                                                       SNKTRIDEANORATKML 17
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     (Longfin squid).
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                                                                                                                                                                                                                                                                                             203
                                                  Created)
Last sequence
Last annotation
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Last annotation update)
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Pred. No. 0.00
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Pred. No. 0.00068;
l; Mismatches 2
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annotation update)
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0.00068;
2;
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ia; Pipoidea;
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ia; Pipoidea; Pipidae;
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  (TrEMBLrel.
                                                     PRELIMINARY;
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SEQUENCE FROM N.A.

Bracher A., Kadlec J., Bet

Bracher Structure of a neur

""-"" 57002) to t'
                                                                                                      InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfann; PF000835; SNAP-25; 1.
SMART; SM00397; T_SNARE; 2.
PROSITE; PS50190; T_SNARE; 2.
SEQUENCE 204 AA; 22771 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2002) to the EMB EMBL; AY092757; AAM18191.1; -
Interpro; IPR000928; SNAP-25.
Interpro; IPR000727; T_SNARE.
Pfam: PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 212 AA; 23816 MW;
                                                                                                                                                                                                                                                                                                                                                                                           QBJIS7; PRELIMINARY;
QBJIS7;
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                     Mashima J., Nagahama M., Hatsuzawa K., Tani K., Kikuchi Horigome T., Yamamoto A., Tagaya M.; "Evidence for the involvement of alpha-SNAP and SNAP-23 of nuclear membrane vesicles."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB033718; BAC06591.1; -.
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; (Amphibia; Batrachia; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Dresbach T., O'Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Loliginidae; Loligo.
NCBI_TaxID=6621;
[1]
                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
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                                                  Local Similarity hes 11; Conserv
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            SNKTRIDEANQRATKML 17
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TNKTRIDEANTKAKKLI 203
                                                    Conservative
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                                                              72.3%;
                                                                                                                                                                                                                                                                                                                                       Chordata;
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neuronal complexin/SNARE
to the EMBL/GenBank/DDBJ d
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22,
23,
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                                                    4;
                                                                                                                                                                                                                                                                                                                         a; Craniata; Vertebrata; Euteleostomi; Mesobatrachia; Pipoidea; Pipidae;
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                                                                  Score 60;
Pred. No.
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Pred. No. 0.
                                                                                                         D034F75E638E8805 CRC64;
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|X
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Best Local S
Matches 17
                                                                                          Query Match
Best Local
                                                                                                                                                                                                Osada N., Hida M., Kusuda J., Tanuma R., Iseki K.
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaqu
libraries.";
thoraties.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ dat
EMBL; AB049852; BAB16738.1;
InterPro; IPR000928; SNAP-25.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 1.
PROSITE; PS50192; T_SNARE; 1.
                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9GM34 PRELIMINARY; PRT; 143 AA. Q9GM34; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Hypothetical 16.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Prim
Cercopithecinae; Macaca.
NCBI_TaxID=9541;
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SMART; SM00397; t_SNARE; 1.
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EMBL; AF091593; AAC64289.1; -.
EFIN; ZDB-GENE-980526-468; snap25a.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
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Bukarydna; Metazoa; Chordata; Craniata; Vert
Acthopterygii; Neopterygii; Teleostei; Osta
Cyprinidae; Danio.
                                                                                                                                                                Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50192; T_SNARE; 1.
NON_TER 1 1
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01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comparison of paralogous
the mammalian lineage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Risinger C., Salaneck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7955;
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17; Conserv
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SNKTRIDEANQRATKML
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                                                                                                                                                           al protein.
143 AA; 1
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(TrEMBLrel. 22, Last annotation update)
associated protein 25.1 (Fragment).
                                                                      Conservative
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neck E., Soderberg
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                                                                                          100.0%;
                                                                                                                                                                16043 MW;
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linkage groups s
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                                                                    Score 83; DB Pred. No. 1.8 D; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini; Cercopithecidae;
                                                                                                                                                                D625DBAAA0893FB0
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                                                                                                                                                                                                                                                                                                                                                                                              from macaque brain
                                                                    1.8e-06;
hes 0;
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Ostariophysi; Cypriniformes;
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                                                                                                               DB 6;
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                                                                                                                                                                CRC64;
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RESULT 5
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EMBL; AF091594; AAC64290.1; -.

EMBL; AF091596; AAC73007.1; -.

ZFIN; ZDB-GENE-980526-392; snap25b.

InterPro; IPR000928; SNAP-25.

InterPro; IPR000727; T_SNARE.

Pfam; PF00835; SNAP-25; 1.

SMART; SM00397; T_SNARE; 2.

PROSITE; PS50192; T_SNARE; 2.

SEQUENCE 203 AA; 22647 MW; 93B759
                                        Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMB Submitted (JUL-2001);
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
InterPro; IPR000727; T_SNARE.
Pfam; PF00035; SNAP-25; 1.
SMART; SM00397; T_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 206 AA; 23336 MW;
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01-NOV-1998
01-OCT-2002
                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created 01-DEC-2001 (TrEMBLrel. 19, Last sec 01-MAR-2003 (TrEMBLrel. 23, Last an Similar to synaptosomal-associated Homo sapiens (Human).
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SYNAPTOSOME-associated p
25,2).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comparison of paralogous the mammalian lineage.";
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Risinger C., Salaneck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNAP25B OR SNAP
                                                                                                                                            TISSUE=Eye;
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                     Q96FM2;
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protein 25.2 (SYNAPTOSOME associated protein
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); Mismatches
          Score 83;
Pred. No.
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                                           E272652C701EA984 CRC64;
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Sequence:
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Gapop 10.0 ,
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83
1 SNKTRIDEANQRATKML 17
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Copyright (c) 1993 - 2003 Compugen
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sp_phage:*
sp_plant:*
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sp_vertebrate:*
sp_unclassified:*
sp_virus:*
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      Q9gm34 macaca fasc
Q9gm34 macaca fasc
Q93579 brachydanio
Q96fm2 homo sapien
Q8axm2 xenopus lae
Q8234 loligo peal
Q8jis7 xenopus lae
Q01389 hirudo medi
Q70377 rattus norv
Q09044 mus musculu
Q9d313 mus musculu
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Q95zk3 caenorhabdi
Q33081 caenorhabdi
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093578 brachydanio
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pseudomonas
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		O85435 pseudomonas	ω	O85438 pseudomonas	085433 pseudomonas	085418 pseudomonas				085420 pseudomonas	Q.	8 cory	Omo	Q9uh61 homo sapien	Q9hat7 homo sapien	. Q9c012 homo sapien	homo	homo	homo		Q9bwu6 homo sapien	O62414 caenorhabdi		Q8zy72 pyrobaculum	O35620 mus musculu	76		085439 pseudomonas

ALIGNMENTS

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RESULT 2
093578
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Best Local Similarity
Matches 17; Conserv
O93578 PRELIMINARY; PRT;
O93578;
O1-NOV-1998 (TrEMBLrel. 08, Created)
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Q9BR45;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DJ1008F16.2.2 (Novel protein (Isoform 2)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; AL023913; CAC34535.1; -.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00035; SNAP-25; 1.
SMART; SM00337; t_SNAP: 1.
PROSITE; PS50192; T_SNARE; 1.
SEQUENCE 80 AA; 8993 MW; Al20C65714D9F071
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                                                                                                                                                                                                                                                                                    61
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Pred. No. 9.7e-07;
Mismatches 0;
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Search Job tim	Db	Qy	В	Оy
Search completed: September 16, 2003, 19:31:53 Job time : 54.5065 secs	189 ITUKADTNEDRIDIANARAKKLIDS 213	181 IMEKADSNKTRIDEANQRATKMLGS 205	129 LQQPTTGAASGGYIKRITNDAREDEMEENLTQVGSILGNLKDMALNIGNEIDAQNPQIKR 188	125 EQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180
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RESULT 14
US-09-942-098-13
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US-09-942-024-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/09942024
Publication No. US20030143650A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ
SEQ ID NO 15
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Fret Protease Assays For Botulinum TITLE OF INVENTION: Serotype A/E Toxins FILE REFERENCE: P-AR 4803
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TYPE: PRT
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TYPE: PRT
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                                                                                                                                   MAISGGFIRRVINDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKAD
                                                                                                                                                                           NADMREAEKNISGMEKCCGICVLPCNKSQSFKEDDGTWKGNDDGKVVNNQPQRVMDDRNG
                                                                                                                                                                                                   NKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDG-VVASQPARVVDEREQ 126
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                                                                   SNEARIAVANORAHOLL 211
                                                                                                                        MMAQAGYIGRITNDAREDEMEENMGQVNTMIGNLRNMALDMGSELENQNRQIDRINRKGE
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                                                                                                                                                                                                                                                                               59.0%; Score 618.5; DB 1 62.9%; Pred. No. 2.5e-50; tive 29; Mismatches 43
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APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: FCT/US00/05988
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 00:124,270
PRIOR APPLICATION NUMBER: 00:124,270
PRIOR APPLICATION NUMBER: 00:124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1718
LENGTH: 213
                                                                                                                                                                                                                                 ; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1718
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Sequence 1718, Application US/09925300; Patent No. US20020151681A1; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Drosophila
US-09-942-098-13
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NUMBER OF SEQ ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13

LENGTH: 212
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                                                                                                                                                        Matches
                                                                                                                                                                        Query Match
Best Local Similarity
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
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                                                                                                                                                        124;
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                                    72 KEAEKNLTDLGKFCGLCVCPCNKLK---SSDAYKKAWG----NNQDGVVASQPARVVDER 124
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                                                                                               SNKTRIDEANQRATKML 203
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RETEKTLTELNKCCGLCVCPCNRTKNFESGKAYKTTWGDGGENSPCNVVSKQPGPVTNGQ 128
                                                                             EEIQQRAHQITDESLESTRRILGLAIESQDAGIKTITMLDEQKEQLNRIEEGLDQINKDM 68
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                                                                                                                                                        Conservative
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                                                                                                                                                                        58.2%;
                                                                                                                                                      ; Score 609.5; DB 1; Pred. No. 1.8e-49; 29; Mismatches 41
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US-09-942-098-16
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                                                          ; ORGANISM: Gallus
US-09-942-098-16
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TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                            CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
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                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09942098 Publication No. US20030143651A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                    TITLE OF INVENTION: Fret Protease Assays For Clostridial TITLE OF INVENTION: Toxins FILE REFERENCE: P-AR 4802
                                                                                                                                                                                                                           APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
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ORGANISM: Gallus gallus
                                                                                      TYPE: PRT
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thes 175;
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              Similarity
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No. US20030143650A1
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95.1%;
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             Score 895;
Pred. No.
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  Mismatches
          No
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              DB 12;
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RESULT 12
US-09-942-098-15
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US-09-942-024-15
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                                                                                                                                        Sequence 15, Application US/099 Publication No. US20030143651A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO. 15
LENGTH: 212
TYPE: PRT
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Best Local
                                                          APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
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FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
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No. US20030143650A1
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Pred. No. 4e-51;
9; Mismatches
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APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Cla
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION UNMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 206
RESULT 7
US-09-942-024-14
; Sequence 14, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
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; ORGANISM: MUS
US-09-942-098-12
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US-09-942-098-12
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; ORGANISM: Rattus
US-09-942-098-7
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Best Local Sim
Matches 206;
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TYPE: PR
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Pred. No. 1.2e-90;
0; Mismatches 0;
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Pred. No. 1.2e-90;
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US-09-942-098-14

Sequence 14, Application US/09942098

Publication No. US20030143651A1

GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Keinandez-Salas, Ester
APPLICANT: Aoki, Keinandez-Salas, Ester
APPLICANT: Aoki, Keinandez-Salas, Ester
APPLICANT: Aoki, Keinandez-Salas, Ester
APPLICANT: Aoki, Keinandez-Salas, Ester
APPLICANTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILLE REFERENCE: P-AR 4802

CURRENT APPLICATION NUMBER: US/09/942,098

CURRENT APPLICATION NUMBER: US/09/942,098

CURRENT FILING DATE: 2001-08-28

NUMBER OF SEO ID NOS: 96

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 14
LENGTH: 203
TYPE: PRT
ORGANISM: Carassius auratus
US-09-942-024-14
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; TYPE: PRT
; ORGANISM: Carassius
US-09-942-098-14
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Acki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays Fo:
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
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Pred. No. 6.5e-80;
7; Mismatches 12;
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Pred. No. 6.5e-80;
7; Mismatches 12
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US-09-942-024-7
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CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 206
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SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 206
TYPE: PRT
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APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Fret Protease Assays For Botulinum TITLE OF INVENTION: Serotype A/E Toxins FILE REFERENCE: P-AR 4803
                                                                                                                                                                                                                                                                                                                     APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
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CURRENT FILING DATE: 2001-08-28
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100.0%; P
afive 0;
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GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
ITITLE OF INVENTION: Fret Protease Assays Formation of Invention: Toxins
ITITLE OF INVENTION: Toxins
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ITITLE OF INVENTION: TOXINS
ITITLE OF INVENTION: USON SERVED ON TOXINS
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GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas,
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Best Local S
Matches 206
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CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 206
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09942098
Publication No. US20030143651A1
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TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
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100.0%; Pred. No. 1.2e-90;
tive 0; Mismatches 0;
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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11: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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Listing first 45 summaries
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US-10-037-182-16	US-09-942-024-88	US-10-128-714-3536	N	US-09-942-098-39	US-09-942-024-39	US-10-128-714-8079	US-10-128-714-3079	US-09-942-098-90	US-09-942-024-90	US-09-738-630-99	US-10-205-219-102	US-10-128-714-3570	US-10-128-714-8570	US-09-952-689-7	US-09-942-098-37	US-09-942-024-37	US-09-942-098-38	US-09-942-098-33	US-09-942-024-38	US-09-942-024-33	US-09-952-689-5	US-09-952-689-3	US-09-952-689-9	US-09-864-761-43057	US-09-925-299-1245	US-09-925-299-1245	US-09-962-360B-12	US-09-962-360B-11
Sequence 16, Appl	,88	3536,	Sequence 320, App	39,	Sequence 39, Appl		3079		90,	99,	Sequence 102, App	Sequence 3570, Ap	Sequence 8570, Ap	Sequence 7, Appli	Sequence 37, Appl	Sequence 37, Appl	38,	33,	Sequence 38, Appl	e 33,	Sequence 5, Appli	Sequence 3, Appli	Sequence 9, Appli	Sequence 43057, A	Sequence 1245, Ap	245	12,	Sequence 11, Appl

ALIGNMENTS

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US-09-942-024-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 96
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 1048; DB 12; Best Local Similarity 100.0%; Pred. No. 1.2e-90; Matches 206; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09942024 Publication No. US20030143650A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
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                                                                                                                                   EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV 120
                                                                     VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180
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IMEKADSNKTRIDEANQRATKMLGSG
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_inverteb
6: sp_mammal:*
5: sp_mhc:*
8: sp_organel.
9: sp_mage:*
10: sp_plant:*
11: sp_rodent:
11: sp_vertebr
13: sp_vertebr
14: sp_urclass
15: sp_virus:*
16: sp_bacteri
17: sp_archeap
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                       Q9br45 homo sapien
Q93578 brachydanio
Q9gm34 macaca fasc
Q9gm34 macaca fasc
Q93579 brachydanio
Q96fm2 homo sapien
Q8df43 vibrio vuln
Q8t34 loligo peal
Q8v219 human respi
Q09717 respiratory
Q09633 human respi
Q8v218 human respi
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Q24902 echinococcu
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ID Q9BR8
AC Q9BR
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DT 01-0
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Interpro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; T_SNARE; 1.
PROSITE; PS50192; T_SNARE; 1.
SEQUENCE 80 AA; 8993 MW; A1
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O93578;
01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                               Q9BR45 PRELIMINARY; PRT; 80 AA.
Q9BR45;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DJ1066B16.2.2 (Novel protein (Isoform 2)).
                                                                                                                                                                                                                                                                                             Babbage A.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AL023913; CAC34535.1; -.
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Similarity 100.0%;
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08P2H7
08P1R5
Q8P1R5
Q9KG18
Q97P37
Q8DNN2
Q8DNN2
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09FZN6
09FZN6
09FEG5
08FEG5
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Q9HFI2
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QBaxm4 xenopus lae
QBrke8 desulfobacu
Q9fzn6 oryza sativ
Q9fzn6 oryza sativ
Q9fown4 xenopus lae
QBfeg5 escherichia
QBzmd9 salmonella
QBzmd9 salmonella
QBzhd1 brachydanio
QBy443 salmonella
QBjhi1 brachydanio
QBy944 caenorhabdi
QBy946 caenorhabdi
QBy9476 streptococc
QBp175 streptococc
QBp175 streptococc
QBp175 streptococc
QBp175 streptococc
QBp175 streptococc
QBdn12 streptococc
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Q9fr53 arabidopsis
Q91pm4 arabidopsis
Q85443 pseudomonas
Q85440 pseudomonas
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085431 pseudomonas
Q8nba4 homo sapien
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RESULT 3

G9GM34

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AC 99GM

AC 99GM

DT 01-W

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DT 01-W

DT 01-C

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SMART; SM00397; t_SNARE; 1.
PROSITE; PS50192; T_SNARE; 1.
Hypothetical protein.
SEQUENCE 143 AA; 16042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Neurosci. Res. 54:563-573(1998).
EMBL; AF091593; AAC64289.1; -
ZFIN; ZDB-GENE-980526-468; snap25a.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 1.
PROSITE; PS50192; T_SNARE; 1.
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MEDLINE-99057281; PubMed-9843147;
MEDLINE-99057281; PubMed-9843147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 16.0 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                      libraries.";
Submitted (OCT-2000) to the
EMBL; AB049852; BAB16738.1;
                                                                                                                                                                                                                                                                                                                                                                                        Osada N., Hida M., Kusuda J., Tanuma I
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Macaca.
NCBI_TaxID=9541;
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InterPro; IPR000727; T_SNARE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                     Conservative
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Pred. No.
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Pred. No. 0.
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Craniata; Ver
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                                                                                                             Length 143;
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EMBL; AF091594; AAC5423007.1;

EMBL; AF091596; AAC73007.1;

ZFIN; ZDB-GENE-980526-392; snap25b

InterPro; IPR000928; SNAP-25.

InterPro; IPR000777; T_NARE.

Pfam; PF00835; SNAP-25; 1.

R SMART; SM00397; t_SNARE; 2.

PROSITE; PS50192; T_SNARE; 2.

PROSITE; PS50192; T_SNARE; 2.
        Query Match
Best Local :
 Matches
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                                       InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 206 AA; 23336 MW;
                                                                                                                                                                                                                      Q96FM2;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                     Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC010647; AAH10647.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of two loci
comparison of paralog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last Sequence update)
01-NOV-1998 (TrEMBLrel. 22, Last annotation update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein
                                                                                                                                     TISSUE=Eye;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                            Similar to synaptosomal-associated
                                                                                                                                                                                                                                                                  Q96FM2
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                                                                                                                                                                               Mammalia; Eutheria;
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Similarity
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llarity 100.0%;
Conservative (
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Metazoa; Chordata;
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23, Last annotation
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; Craniata; Vertebrata;
Teleostei; Ostariophysi
Score 39; DE
Pred. No. 0.8
); Mismatches
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Pred.
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Catarrhini;
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                                          E272652C701EA984 CRC64;
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                   DB 4;
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01-MAR-2003 (TrEMBLrel. 2
Hypothetical protein.
VV10381.
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O8DF43;
O1-MAR-2003
O1-MAR-2003
O1-MAR-2003
                                                                         Piam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 212 AA; 23816 MW;
                                                                                                                                   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; AY092757; AAM18191.1; -.
InterPro; IPR000928; SNAP-25
InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                           SEQUENCE FROM N.A. Dresbach T., O'Con "Squid SNAP25.";
                                                                                                                                                                                                                                                  Bracher A., Kadlec J., "X-ray structure of a r Submitted (APR-2002) to
                                                                                                                                                                                                                                                                                                                                         SNAP25 fusion protein.
Loligo pealeii (Longfin squid).
Eukaryota; Metazoa; Mollusca; Cephalopoda;
Decapodiformes; Loliginidae; Loligo.
                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TIEMBLIEL 21,
01-JUN-2002 (TIEMBLIEL 21,
01-CCT-2002 (TIEMBLIEL 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Vibrio vulnificus Submitted (DEC-2002) to the EMBL/GenBank/DDBJ EMBL; AE016798; AA008905.1; -
Hypothetical protein; Complete proteome. SEQUENCE 162 AA; 18029 MW; 65272C082012A47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhee J.H., Kim S.Y., Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio vulnificus.
Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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75.0%;
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                  Score 32; DB Pred. No. 32; 2; Mismatches.
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Last sequence update)
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65272C082012A474 CRC64;
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Best Local :
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01-MAR-2002
                SEQUENCE FROM N.A
                                                                                                                                               STRAIN=S2 ts1C;
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NCBI_TaxID=11250;
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"Identification of mutations contributing to the reduced a modified strain of respiratory syncytial virus."; Vaccine 14:1637-1646(1996).
                                                 Tolley K.P., Marriott A.C., Simpson Longhurst S.J., Evans J.E., Johnson Pringle C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-beijing;
Zhao L.Q., wang Z.L., Geng X.H., Qian Y., Deng Zhao L.Q., the EMBL/GenBank/DDBJ Submitted (NOV-2001) to the EMBL/GenBank/DDBJ EMBL; AF453422; AAL50987.1; -IPR003487; Prenumo_phosprot.

Pfam; PF02478; Pneumo_phosprot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-beijing;
MEDLINE=21364133; PubMed=11471029;
Zhao L.O., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,
Wang L.T., Liu C.O., Chang R.X.;
"Sequence analysis of phosphoprotein genes of respiratory syncytial virus field strains isolated in China.";
Chung Hua Shih Yen Ho Lin Chuang Ping Tu Hsueh Tsa Chih
                                                                                                MEDLINE=97185152; PubMed=9032893;
                                                                                                                                                                              Viruses; ssRNA negative-strand Paramyxoviridae; Pneumovirinae;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                           Human respiratory syncytial virus. Viruses; ssRNA negative-strand virus-paramyxoviridae; Pneumovirinae; Pn. NCBI_TaxID-11250;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                      Q04161
Q04161;
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Submitted (OC
EMBL; U39661;
                                                                                                                                                                                                                                                                         Submitted (OCT-1995) to the EMBL/GenB
EMBL; U39662; AAC57023.1; -
InterPro: IPR003487; Pneumo_phosprot.
Pfam; PF02478; Pneumo_phosprot; 1.
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97185152; PubMed-9032893;
Tolley K.P., Marriott A.C., Simpson Longhurst S.J., Evans J.E., Johnson Pringle C.R.;
          SEQUENCE
                                                                             Phosphoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                  Easton A.J.;
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                                                                                                                                                                                                                                                                                                                                                       "Identification of mutations conta modified strain of respiratory Vaccine 14:1637-1646(1996).
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Viruses; ssRNA negative-strand viruses; Mono
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCHI_TaxID=11250;
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InterPro; IPRO03487; Pneumo_phosprot.
Pfam; PF02478; Pneumo_phosprot; 1.
SEQUENCE 241 AA; 27134 MW; 3EED90
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                                               viruses; Mononegavirales;
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EMBL; M67450; AAA47419.1;
InterPro; IPR002048; EF-hand.
InterPro; IPR003487; Pneumo_phosprot.
Pfam; PF02478; Pneumo_phosprot; 1.
PROSITE; PS00018; EF-HAND; 1.
NON_TER 241 241
Q8V218
Q8V218;
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Q8UYD5;
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Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng
Wang L.T., Liu C.,O. Chang R.X.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ
EMBL; AF453423; AAL50980.1;
EMBL; AF453423; AAL50988.1;
InterPro; IPR003487; Pneumo_phosprot.
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                                                                                                                                                                   SEQUENCE
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MEDLINE-21364133; PubMed-11471029;
Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., D
Wang L.T., Liu C.Q., Chang R.X.;
"Sequence analysis of phosphoprotein genes
virus field strains isolated in China.";
Chung Hua Shih Yen Ho Lin Chuang Ping Tu Hs
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                                                                                                                                                                                                                                                                                                                                                                                                         Human respiratory syncytial virus. Viruses; ssRNA negative-strand vir
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MEDLINE-92197000;
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NCBI_TaxID=11250;
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Wang L.T., Liu C.Q., Chang R.X.;
"Sequence analysis of phosphoprotein genes
virus field strains isolated in China.";
Chung Hua Shih Yen Ho Lin Chuang Ping Tu Ha
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                                                                                                                                                     MEDLINE=97187925; PubMed=9
Crowe J.E. Jr., Firestone
Murphy B.R.;
"Acquisition of the ts phe
                                                                                                                                                                                                                                                                                                               subgroup A cold-passaged (cp) live attenuated virus vaccine Virology 225:419-422(1996).
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Firestone C.Y., Whitehead S.S., Collins
Crowe J.E. Jr.;
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Pfam; PF02478; Pneumo_phosprot 1
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NCBI_TaxID-11250;
                       STRAIN-A
                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequence analysis of the respiratory syncytial virus subgroup A cold-passaged (cp) temperature sensitive (ts) cpts-24-live attenuated virus vaccine candidate.";
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                                                                           LLON OF the ts phenotype by a chemically mutagenized cold-
human respiratory syncytial virus vaccine candidate results
acquisition of a single mutation in the polymerase (L) genenes 13:269-273(1996).
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viridae; Pneumovirinae; Pneumovirus.
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AA; 27226 MW;
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.L., Geng X.H., Q
Q., Chang R.X.;
                                                                                                                                                                                             PubMed=9035372;
irestone C.Y., Whitehead
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75.0%;
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Last sequence update)
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Pred. No.
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RESULT 15
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Best Local S
Matches
  Query Match
Best Local Similarity
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                                                                                            SMART; SI
PROSITE;
                                                                                                                                   PRINTS;
ProDom;
                                                                                                                                                                             Parasitology 122:281-287(2001).
EMBL; AF207904; AAF19966.1; -.
HSSP; P29312; 1A37.
InterPro; IPR000308; 14-3-3.
Pfam; PF00244; 14-3-3; 1.
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                                                                                                                                                                                                                                                                                                                                                                        STRAIN-sheep;
MEDLINE=21182697; PubMed=11289064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Echinococcus granulosus.
Eukaryota; Metazoa; Platyhelminthes; Ce:
Eukoryota; Metazoa; Platyhelminthes; Ce:
Cyclophyllidea; Taeniidae; Echinococcus
NCBI_TaxID=6210;
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                   Siles-Lucas M., Nunes Comparative analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9U408
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                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                            metacestodes
                                                                                                                                                                                                                                                                                                                      Echinococcus
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                                                                                       S; PR00305; 1433ZETA.
m; PD000600; 14-3-3; 1
; SM00101; 14_3_3; 1.
TE; PS00797; 1433_2; 1
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    79.5%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                      C.P., Zaha A.;
of the 14-3-3
                                                                                                                                                                                                                                                                                                                 and Echinococcus
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    Score
Pred.
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DB
62;
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2003			1;
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			0;
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Retession: G65060
A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                            probable glucarate dehydratase ygcX [imported] - Escherichia coli (strain 0157:H7, C;SpecLes: Escherichia coli
C;SpecLes: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: H85929
C;Accession
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H85929
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gen/A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G91084
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 
C;Accession: G91084
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G91084
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                                   A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: H85929
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C;Superfamily: glucarate dehydratase
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A; Residues: 1-446 <HAY>
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A; Residues: 1-446 <BLAT>
A;Status: preliminary
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Local Similarity 75.0%;
les 6; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.98;
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Pred. No. 57;
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                                                                                                                                                                                                         J.D.; Rose, D.J.; Mayhe
Potamousis, K.; Apodaca
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A;Molecule type: DNA
A;Residues: 1-446 <STO>
A;Cross references: GB:AE005174; NID:g12517262; PIDN:AAG57900.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Gene: YgCX
C;Superfamily: glucarate dehydratase
밁
                      QУ
                                                               Query Match
Best Local (
                                                    Matches
373 EGNQRLTK 380
                                                  l Similarity
6; Conserv
                        1 EANQRATK 8
                                                 Conservative
                                                                76.9%;
75.0%;
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                                                                Score 30;
Pred. No.
                                                    Mismatches
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                                                    2,
                                                                           Length 446
                                                    Indels
                                                    0,
                                                    Gaps
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Search completed: September 16, 2003, 19:30:46 Job time: 3.07792 secs

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A;Reference number: Z21890
A;Accession: T39913
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 365-2337 <LYN>
A;Residues: 365-2337 <LYN>
A;Cross-references: EMBL:AL049558; PIDN:CAB40167.1; GSPDB:GN00067; SPDB:SPBC216.07c
R;Seeger, K; Harris, D; Wood, V.; Rajandream, M.A.; Barrell, B.G.
R;Seeger, K; Harris, Di Wood, V.; Rajandream, M.A.; Barrell, B.G.
R;Seeger, K; Harris, D; Wood, V.; Rajandream, M.A.; Barrell, B.G.
R;Seeger, K; Harris, D; Wood, V.; Rajandream, M.A.; Barrell, B.G.
A;Cross-reference number: Z1938
A;Accession: 740577
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-398 <SEE>
A;Cross-references: EMBL:AL035216; PIDN:CAA22805.1; GSPDB:GN00067; SPDB:SPBC646.01c
A;Experimental source: strain 972h-; cosmid c646
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
G96536
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A;Reference number: S07428; MUID:88323192; PMID:3414184
A;Accession: S07428
A;Molecule type: mRNA
A;Residues: 1-241 <LOP>
A;Cross-references: EMBL:M22644; NID:g333949; PIDN:AAA47415.1;
C;Genetics:
A;Gene: P
C;Superfamily: respiratory syncytial virus phosphoprotein P
C;Keywords: phosphoprotein
                                                                                                                                                                                                                                                                          hypothetical protein F2J10.9 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_chang.C;Accession: G96536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: SPBC646.01c
A;Map position: 2
C;Superfamily: yeast TOR2 protein
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 15-Sep-2000 #text_change 06-Oct-2000
C;Accession: T39913; T40577
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75.0%;
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1.8e+02;
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A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: GB:L22020; NID:g431296;
                                                                                                                       A;Title: Evolutionary conservation of synaptosome-associated A;Reference number: A49513; MUID:94043281; PMID:8226991 A;Accession: 150552 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                         synapse protein marbled electric ray cyspectes: Torpedo marmorata (marbled cyspectes: Torpedo marmorata (marbled Cybate: 11-Sep-1996 #sequence_revision Cyaccession: I50552
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Genome: chloroplast
C;Superfamily: H+-transporting ATP synthase chain
C;Keywords: ATP biosynthesis; chloroplast; hydrola
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T07210
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A;Accession: G96536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2513 <STO>
A;Cross-references: GB:AE005173; NID:g8569097; PIDN:AAF76442.1; GSPDB:GN00141
                                                                                                                                                                               R;Risinger, C.; Blomgvist, A.G.; Lundell, I.; Lambertsson, J. Biol. Chem. 268, 24408-24414, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57857.1; PID:g2224373C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-175 <W
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                                        Query Match
Best Local
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Torpedo marmorata (marbled electric ray)
בייחיר *מסחוסחכפ_revision 13-Sep-1996 #text_change 21-Jul-2000
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6; Conser
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201

EANKHATK

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nerve terminal protein - human
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Species: 1948-1998 #sequence_revision 29-May-1998 #te:
C:Accession: 167823
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isofe
A;Reference number: 153735; MUID:94156217; PMID:811262:
A;Accession: 167823
A;Residues: 17823
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: GB:L19761; NID:g307427; PIDN:AAC37:
C:Genetics:
A;Gene: GDB:SNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J. Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Accession: A37861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:SNAP
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2
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R; Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
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C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
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A; Residues: 1-206 < RES>
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A;Molecule type: mRNA
A;Residues: 1-206 <CAT
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                                                                                                                                 clones encoding two different isoforms I53735; MUID:94156217; PMID:8112622
                                         GB:L19761; NID:g307427; PIDN:AAC37546.1; PID:g307428
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100.0%; Pred. No.
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C; Superfamily: 1
C; Keywords: pho:
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       Villanueva, N.;
249-262, 1988
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phosphoprotein P - human respiratory syncytial virus (strain Long) C;Species: human respiratory syncytial virus C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16 C;Accession: S07428
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C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-assoc:
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A;Map position: 20p11.2-20p11.2
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence analysis of the respiratory syncytial A;Reference number: A04037; MUID:85033973; PMID:6548527 A;Accession: A04037
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                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M11486; GB:K02719; NID:g333925; PIDN:AAB59853.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-241 <SAT>
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A; Residues: 1-206 < OYL>
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Mismatches
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

RESULT 1 I50481

synapse protein SNAP-25 - goldfish C; Species: Carassius auratus (goldfish) C; Date: 13-Sep-1996 #sequence_revision

13-Sep-1996 #text_change 21-Jul-2000

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tetraploid goldfish

C; Date: 17 07 1.0 C; Date: 17 07 1.0 C; Date: 17 07 1.0 C; Accession: 150481
C; Accession: 150481
R; Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A; Title: Multiple loci for synapse protein SNAP-25 in the companience of the compa

A; Cross-references: C; Genetics:

GB:L22976; NID:g349430; PIDN:AAA16538.1; PID:g349431

from GB/EMBL/DDBJ

A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-203 <RIS>

synapse protein SNAP-25 - goldfish
C; Species: Carassius auratus (goldfish)
C; Species: Carassius auratus (goldfish)
C; Accession: 150480
C; Accession: 150480
R; Alsinger; C; Larhammar; D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A; Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfis A; Accession: 150480
A; Accession: 150480
A; Status: preliminary; translated from GB/EMBL/DDBJ RESULT I50480 В QΥ A;Cross-references: GB:L22973; C;Genetics: A; Molecule type: mRNA A; Residues: 1-204 < RIS> Вþ QΥ A; Gene: A; Gene: SNAP-25 Matches Query Match Best Local Matches Query Match Best Local S SNAP-25 191 EANQRATK 198 192 EANQRATK 199 1 EANQRATK Similarity 8; Conserv Similarity 8; Conserv EANQRATK 100.0%; ilarity 100.0%; Conservative Conservative œ 8 100. .0%; 0%; NID: g349426; 0; 0, Score 39; DB 2 Pred. No. 0.22; ; Mismatches Score 39; I Pred. No. 0. Mismatches PIDN: AAA16537.1; DB . า. 22; 2: ν, 0; Length 203; Length 204; Indels Indels tetraploid goldfish. PID:g349427 0; 0; Gaps Gaps 0 0;

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FITLE OF INVENTION: Fret Protease Assays For Botulinum;
FITLE REFERENCE: P-AR 4803;
CURRENT APPLICATION NUMBER: US/09/942,024;
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEO ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 44
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence;
PATURE: OPERTURE: OPERT
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Matches
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CURRENT FILLING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 96
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 94

LENGTH: 16
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CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 91
LENGTH: 16
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Fret Protease Assays For Clostridial TITLE OF INVENTION: Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Steward, Lance E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Fret Protease Assays For Clostridial TITLE OF INVENTION: Toxins FILE REFERENCE: P-AR 4802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fernandez-Salas, Ester APPLICANT: Aoki, Kei Roger TITLE OF INVENTION.
                                                                                                                                                         OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: 1
OTHER INFORMATION: Xaa-DABCYL modified lysine
NAME/KEY: MOD_RES
LOCATION: 16
OTHER INFORMATION: Xaa-EDANS modified glutamate
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LOCATION: 16
OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
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LOCATION: 1
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OTHER INFORMATION: synthetic peptide
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US-09-942-024-30
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                                              Sequence 44, Application US/09942024 Publication No. US20030143650A1 GENERAL INFORMATION:
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Matches 8
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SEQ ID NO 31
LENGTH: 17
TYPE: PRT
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Publication No. US20030143650A1
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APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
APPLICANT: Steward, Lance E. APPLICANT: Fernandez-Salas, APPLICANT: Aoki, Kei Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Fret Protease Assays For Botulinum TITLE OF INVENTION: Serotype A/E Toxins FILE REFERENCE: P-AR 4803
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APPLICANT: Fernand
APPLICANT: Aoki, K
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CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
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                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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8; Conser
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 Fernandez-Salas, Ester
Aoki, Kei Roger
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Aoki, Kei Roger
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Pred. No. 0.07;
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CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-942-024-29
RESULT 9
US-09-942-024-94
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Best Local S
Matches 8
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Publication No. US20030143650A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 91
LENGTH: 16
TYPE: PRI
ORGANISM: Artificial Sequence
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Best Local
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Publication No.
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CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
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LOCATION: (0)...(0)
OTHER INFORMATION: at the C-terminal
                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: 1
OTHER INFORMATION: Xaa-fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 16
OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
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Pred. No. 0.066;
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Pred. No. 0.066;
Mismatches
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; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-94
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                                                                  Query Match
Best Local S
Matches 8
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Best Local S
Matches 8
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CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 16
TYPE: PRT
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CURRENT FILING DATE: 2001-08-28
NUMBER OF SEO ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 94
LENGTH: 16
TYPE: PRT
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APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas,
APPLICANT: Aoki, Kei Roger
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: AOK1, Kei Roger
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OTHER INFORMATION: Xaa-DABCYL modified lysine
NAME/KBY: MOD_RES
LOCATION: 16
OTHER INFORMATION: Xaa-EDANS modified glutamate
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OTHER INFORMATION:
NAME/KEY: MOD_RES
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8; Conserv
EANQRATK 15
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Aoki, Kei Roger
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ilarity 100.0%;
Conservative 0
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ilarity 100.0%;
Conservative 0
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Pred. No. 0.066;
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Pred. No. 0.066;
                                                                    Mismatches
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RESULT 11 US-09-942-098-91 ; Sequence 91, Application US/09942098 ; Publication No. US20030143651A1

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Query Match
Best Local Similarity
Watches 8; Conserve
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; ORGANISM: Homo sapiens
US-09-942-024-27
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US-09-942-024-27
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Best Local S
Matches 8
                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
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CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                       SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
APPLICANT: April Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
TITLE OF INVENTION: Fret Protease Assays For Clostridial TITLE OF INVENTION: Toxins FILE REFERENCE: P-AR 4802 CURRENT APPLICATION NUMBER: US/09/942,098 CURRENT FILING DATE: 2001-08-28 NUMBER OF SEQ ID NOS: 96 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 27 LENGTH: 13
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SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
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Pred. No. 0.0
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APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
ITILE OF INVENTION: Fret Protease Assays For Botulinum
ITILE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 15
TYPE: PRI
TYPE: 
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US-09-942-098-28
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                                                                                                                 Query Match
Best Local S
Matches 8
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 15
TYPE: PRT
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Publication No.
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Best Local Similarity 100
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Steward, Lance E. APPLICANT: Fernandez-Salas, Ester APPLICANT: AOK1, Kei Roger TITLE OF INVENTION: Fret Protease / TITLE OF INVENTION: Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: P-AR 4802
                           1 EANQRATK 8
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No. US20030143650A1
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Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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US-09-942-024-91
US-09-942-024-94
US-09-942-038-91
US-09-942-038-94
US-09-942-038-94
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ALIGNMENTS

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RESULT 2
US-09-942-098-1
Sequence 1, Application US/09942098
Publication No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
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Publication No. US20030143650A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
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LENGTH: 8
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APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays :
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
FEATURE:
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Search completed: September 16, 2003, 19:26:24 Job time: 5.71429 secs
                                                                                                                                                                                                                                                                                   CC This sequence corresponds to residues 170-206 of the human 25 kD CC synaptosomal associated protein (SNAP-25), and is a inhibitory agent of CC the invention. The agents of the invention inhibit secretion of CC neurotransmitter from neuronal cells and is an excitation-secretory CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which CC correspond substantially to any one of AAW30097-W30102, or more CC generally any (I) that inhibits 50% of catecholamine secretion from CC bovine chromaffin cells at a concentration of 10 microM, especially 0.25 cmicroM, or less. (I) are used, as a replacement for Clostridium toxin, to CC inhibit release of neurotransmitters from synaptic vesicles, specifically CC for reducing muscle spasticity. Also (I) may be labelled to allow in CC unaging of intracellular distribution of (I). Compounds for CC delivering the drug to neural cells provide targeted drug delivery, e.g. CC of substance P to brain tumours for induction of apoptosis. Unlike the CC neurotoxins, (I) are not toxic or immunogenic and are more readily available. Their therapeutic effect lasts for several days or weeks, so lower doses or less frequent treatments are required.
                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                    Sequence
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25 EANQRATK 32
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                                                                                      Homo sapiens
                                                                                                                                            synaptosomal associated
                                                                                                                                                                 Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
                                                                                                                                                                                                                                                                                     Neurotransmitter secretion
                                                                                                                                                                                                                                                                                                                                                 06-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW30099 standard;
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .0%;
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                                                                                                                                                                                                                                                                                        inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating muscle
to neural cells
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Qy
                                     Matches
                                                     Best
                                                                   Query Match
                                                                                                                                                                                                                                                                                                       This sequence corresponds to residues 181-206 of the human 25 kD synaptosomal associated protein (SNAP-25), and is a inhibitory agent the invention. The agents of the invention inhibit secretion of neurotransmitter from neuronal cells and is an excitation-secretory uncoupling peptide (I) of at least 20 amino acids (aa) all of which correspond substantially to any one of AAW30097-W30102, or more generally any (I) that inhibits 50% of catecholamine secretion from
                                                                                                                                 microm, or less. (I) are used, as a replacement for Clostridium toxin, to inhibit release of neurotransmitters from synaptic vesicles, specifically for reducing muscle spasticity. Also (I) may be labelled to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering the drug to neural cells provide targeted drug delivery, e.g. of substance P to brain tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not toxic or immunogenic and are more readily available. Their therapeutic effect lasts for several days or weeks, so lower doses or less frequent treatments are required.
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Excitation-secretory uncoupling peptide(s) for inhibiting neuro:transmitter release - used particularly for treating spasticity, and for delivering drugs specifically to neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-1996;
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                                                                                                                                                                                                                                                                                         bovine chromaffin cells at a concentration of 10 microm, especially 0.25
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                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                     Similarity
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                                                                                                       26 AA;
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALIFORNIA
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   8
                                                   100.
                                                     .0%;
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                                   0;
                                                     Score 39;
Pred. No.
                                   Mismatches
                                                     0.18;
                                                                   DB 18;
                                   0;
                                                                   Length
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to neural cells
                                                                     26;
                                   0;
                                                                                                                                                                                                                                                                                                                                                                                              agent
                                   Gaps
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14 1 EANQRATK EANQRATK 21

В

AAW30097 standard; peptide; 37

AAW30097;

06-APR-1998 (first entry)

Neurotransmitter secretion inhibitor #1

RESULT 15
AAW30097
ID AAW30
XX AAW30
XX AAW30
XX Neurc
XX Neurc
KW Neurc
KW excit
KW bovit
KW bovit
KW synat
XX weururransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25. Homo sapiens

W09734620-A1

18-MAR-1997; 97WO-US04393

18-MAR-1996; 96US-0013599

(REGC) UNIV CALIFORNIA.

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RESULT 11
ABG69065
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                                        Matches
                                                       Query Match
Best Local
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Matches
                                                                                                                                    The invention relates to a nucleic acid molecule encoding a botulinum neurotoxin light chain (BoNT LC) serotype A, where the DNA has a sequence that is expressible in a host organism other than Clostridium, or has a total A+T content that is less than about 70% The BoNT LC protein is useful in vaccination against botulism, for eliciting protective immunity in a mammal, for treating dystonias, spasticity, pain, ocular motility, facial dyskinesias, stiff-person syndrome, bladder dysfunction, segmental myoclonus, hyperkinetic disorders, cosmetic treatment of facial wrinkles, conditions characterised by hyperactivity of the lower motor neuron, and to control autonomic nerve function or tiptoe-walking due to stiff muscles common in children with cerebral palsy. The sequences are also useful for screening for botulinum neurotoxin inhibitors. This sequence represents a human polypeptide C-terminal fragment, used in the scope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Botulinum neurotoxin light chain; BoNT LC; botulism; dystonia; pain; spasticity; ocular motility; facial dyskinesia; stiff-person syndrome; bladder dysfunction; segmental myoclonus; hyperkinetic disorder; human; cosmetic treatment; facial wrinkle; cerebral palsy; analgesic; relaxant; lower motor neuron hyperactivity; autonomic nerve function; muscular;
                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid molecule encoding botulinum neurotoxin light chain serotype A, useful for producing the neurotoxin for vaccination against botulism, comprises sequence expressible in host other than Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2000;
20-JUL-2001;
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                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG69065;
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                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-575192/61.
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                                        Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                           25; Page 62;
EANQRATK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jensen M;
                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-246774P.
; 2001US-0910186.
; 2001US-311966P.
                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial.
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                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                          166pp; English.
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                                                     Score 39;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATERIAL COMMAND
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                                         Mismatches
                                                     0.12;
                                                                     DВ
                                                                    23;
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                                                                 Length 17;
                                        Indels
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                                         Gaps
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RESULT 13
AAW30100
ID AAW30
XX
AC AAW30
XX
DT 06-AF
XX
DE Neurc
XX
KW Neurc
KW excit
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AAB15586
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                                                                                                                                                                                      Qγ
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                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                The invention relates to new peptides comprising 3-30 contiguous amino acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated protein 25). The peptides AAB15581-B15586 represent examples of the peptides of the invention. The peptides have neuronal exceytosis inhibitory activity and are used for treatment of facial wrinkles and asymmetry and pathological neuronal exocytosis-mediated pathological disorders and alterations manifested e.g. by spasms and neurological and neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                           06-APR-1998
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fernandez Ballester
Viniegra Bover S, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator; SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human SNAP-25 N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2001
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                                                                                                         AAW30100
                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 34; 40pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                New peptides containing amino acid sequences treatment of neurological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blanes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200064932-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurodegenerative disorder.
                                  Neurotransmitter secretion inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perez Paya E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIPO-) LIPOTEC SA.
                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                              Similarity
8; Conserv
                                                                                                       standard; peptide;
                                                                                                                                                                 EANORATK
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                                                                                                                                                                                                                                                              19
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                                                                                                                                                                                                              Conservative
                                                          (first entry)
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                                                                                                                                                                                                                                                              ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99ES-0000844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Llobregat Hernandez MM, Gil Tebar AI;
ter GJ, Planell Cases RM, Ferrer Montiel AV;
, Gutierrez Perez LM, Carbonell Castell T;
                                                                                                                                                                 17
                                                                                                                                                                                                                         100.0%;
                                                                                                         20
                                                                                                                                                                                                               0;
                                                                                                                                                                                                                            Score 39;
Pred. No.
                                                                                                         A
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                                   #4.
                                                                                                                                                                                                                            0.13;
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                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                    contiguous amino
                                                                                                                                                                                                                                                                                                                                                                                                                               proteins for
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Neurotransmitter secretion; inhi excitation-secretory uncoupling

inhibitor; neuronal cell; synaptic

vesicle;

catecholamine

peptide;

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RESULT 9
AAY44057
ID AAY4057
AC AAY
XX AAY
AC AAY
XX DT 18-
XX Enz
XX Enz
KW fluw
KW hydd
XX Home
OS Syni
XX 12-
XX 06-
XX 06-
XX 06-
XX 05-
PF 06-
XX US5
XX US5
PF US5
XX US5
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. Botulinum toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the peptide at different time points; and measuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of type A botulinum toxin.
                                                                                                                                                   The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. Botulinum
                                                                                                                                                                                                                                                                          Disclosure; Column 9; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis; fluorescamine; detection; human; synaptosomal protein; SNAP25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                   The invention relates to an
                                                                                                                                                                                                                                                                                                                                    Quantitation of type A botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSA ) US
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                                                                              The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. Botulinum toxin A has been shown to cleave the synaptosomal neurotransmitter peptide sNAP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022 * 744076) of the SNAP25 peptide (AAY44021) amino acids 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the peptide at different time points; and measuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured under similar conditions.
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of type A botulinum for
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                                                                                                                         Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
fluorescamine; detection; human; synaptosomal protein; SNAP25;
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Synthetic.
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                                                                                                                                                                  Human SNAP25 (amino acids 187-203) analogue M16A.
              12-OCT-1999.
                                                                                                              hydrolysis; amino group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                            06-NOV-1996;
                                                                                                                                                                                           US5965699-A
                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                       Enzymatic assay; quantitation; type A botulinum neurotoxin; fluorescamine; detection; human; synaptosomal protein; SNAP;
                                                                                                                                                                                                                                                                                                                Human SNAP25 (amino acids 187-203) analogue
                                                                                                                                                                                                                                                                                                                                         18-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               AAY44056 standard; peptide; 17
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                                                      Bostian KA,
                                                                                                                                     06-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                            hydrolysis; amino group.
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                                                                                 SEC OF ARMY.
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ilarity 100.0%;
Conservative 0
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                                                      Schmidt JJ
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                                                                                                           96US-0743894
                                                                                                                                     96US-0743894
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Pred. No.
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                                                                                                                                                                                                                                                                        oxin; proteolysis;
SNAP25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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D)

Quantitation of type A botulinum toxin

WPI; 1999-579939/49

Human SNAP25 (amino acids 187-203) analogue

#18

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RESULT 4
AAY44021
AAY44021
AAY44021
AAY
AAC AAC AAY
AA
RESULT 5
AAY44039
ID AAY4
XX
AC AAY4
XX
DT 18-J
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. The method comprises adding an analogue (e.g. AAV44022-Y44076) of this peptide (which represents amino acids 187-203 of the human synaptosomal protein SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the peptide at different time points; and measuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of
  18-JAN-2000
                                                          AAY44039;
                                                                                                            AAY44039 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Column 4; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quantitation of type A botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bostian KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type A botulinum toxin.
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Pred. No. 0.12;
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Best Local S
Matches 8
                                                                       Human
                                                                                                                               AAY44044;
                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                  18-JAN-2000
                                                                                                                                                         AAY44044 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 7-8; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quantitation of type A botulinum toxin
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                                                                       SNAP25
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                                                                                                                                                                                                                                                                                        Similarity
8; Conser
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                                                                                                                                                                                                                                                                                        Conservative
                                                                      (amino
                                                                                                 (first entry)
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                                                                      acids 187-203) analogue M16X.
                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                        0;
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Pred. No. 0.1
); Mismatches
                                                                                                                                                                                                                                                                                                    0.12;
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Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis; fluorescamine; detection; human; synaptosomal protein; SNAP25;

amino

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RESULT 2
AAY44058
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Best Local S
Matches 8
type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. Botulinum toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, the stopping hydrolysis of the peptide at different time containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           botulinum neurotoxin type A using fluorescamine detection. Botulinum toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the peptide at different time points; and measuring the amount of hydrolysis at each time point by combining with label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of type A botulinum toxin.
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                                                                                                                                                          Disclosure; Column
                                                                                                                                                                                    Quantitation of type A botulinum toxin
                                                                                                                                                                                                                        WPI; 1999-579939/49
                                                                                                                                                                                                                                                                                   (USSA ) US
                                                                                                                                                                                                                                                                                                                  06-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis; fluorescamine; detection; human; synaptosomal protein; SNAP25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hydrolysis; amino
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8; Conser
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                                                                                                                                                                                                                                                                                    SEC OF ARMY.
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Marity 100.0
Conservative
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                                                                                                                                                         9; 28pp; English.
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by determining the proteolytic activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28pp; English
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                       type A botulinum toxin, by determining the proteolytic activity of to botulinum neurotoxin type A using fluorescamine detection. Botulinum toxin, by determining the proteolytic activity of toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 between residues 197-198. The method comprises adding amino acids 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the peptide at different time points; and measuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of type A botulinum toxin.
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                                                                                                                                                                                                                                                                                                 Quantitation of type A botulinum toxin
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Quantitation of type A botulinum toxin
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Synthetic.
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                                                                                  Bostian KA, Schmidt JJ
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                                                             SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE; toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis; synaptosomal-associated protein; mouse; mutant; mutein; N-ethylmaleimide-sensitive fusion protein;
                                                                                                                                                             Synaptosomal-associated
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                                                                                                                                                                                                                                                                      AAU00256 standard; Protein;
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Synthetic
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                                                  NSF-attachment protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                VDEREQMA ISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAMGNNQDGVVASQPARV
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                                                                                                                                                                                               (first entry)
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Pred. No. 8.3e-90;
                                                  receptor
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                                                                                                                                                           SNAP25,
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                                                                                                                                                         mutant Q197A/R198A.
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VDEREQMAISGGFIRRYTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR VDEREQMAISGGEIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR

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                                                                                                                                    method of treating a patient suffering from poisoning or at risk of CC method of treating a patient suffering from poisoning or at risk of CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) CC to a cell of the patient, where the SNARE is resistant to proteolysis by CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of CC treating a patient in need of inhibition of SNARE-dependent exocytosis comprises CC supplying a fragment, variant, fusion or derivative of a SNARE or a recombinant polynuclectide encoding the SNARE or an inhibitory SNARE or a recombinant polynuclectide encoding the SNARE is CC supplying a fragment of a medicament for the treatment of a patient CC suffering from poisoning or at risk of poisoning by clostridial toxin, CC e.g. from botulism or tetanus. The fragment, variant, fusion or CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant could be considered by constitution of SNARE or of an inhibitory SNARE, or a recombinant CC polynuclectide encoding either of these SNARE polypeptides are useful in the manufacture of medicament for the treatment of a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis from a cell capable of taking the paritent out of critical state.
                                                                                   Query Match
Best Local
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents the amino acid sequence of synaptosomal-
associated protein, SNAP25, mutant Q197A/R198A, used in a new
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating a patient suffering from poisoning a clostridial toxin, e.g. botulism, comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents the amino acid
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                 MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
                                                                                                                                                                 present sequence is not shown in the rom the mouse SNAP-25 sequence given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Sullivan
                                                                                                                                    206 AA;
                                                                     Conservative
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99.08;
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No. le-89;
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                     The sequence represents the amino acid sequence of synaptosomal-associated protein, SNAP25, mutant Q197K/R198H, used in a new method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can be used in a method of treating a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis comprises supplying a fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is useful in the manufacture of a medicament for the treatment of a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating a patient suffering from poisoning or at risk of poisoning a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE -
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toxin-inhibitory SNARE;
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poisoning or at risk of poisoning by
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ARE; botulism; tetanus; SNARE-dependent exocytosis;
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RESULT 14
AAUU2171
ID AAUU22171
AAUU22171
AC AAUU22
XX SNAP
AC SYNAE
XX SYNAE
XX SNAP
KW SYNAE
KW SYNA
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxin-inhibitory SNARE; botulism; tetanus; SNAR synaptosomal-associated protein; mouse; mutant;
                          WPI; 2001-226739/23
                                                                          Dolly JO,
                                                                                                                                                                                20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-ethylmaleimide-sensitive fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synaptosomal-associated protein, SNAP25, mutant R198T/L203A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU02171 standard;
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                                                                                                                                                                                                                                                                                     15-MAR-2001
                                                                                                                                                                                                                                                                                                                                        WO200118038-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204;
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                                                                                                                             IMPERIAL COLLEGE INNOVATIONS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                             O'Sullivan GA,
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                                                                                                                                                                                                                                   2000WO-GB03196
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203
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99.08;
                                                                                                                                                                                                                                                                                                                                                                                      "Wild-type Leu substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Wild-type Arg substituted
                                                                             Mohammed N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1039; DI
Pred. No. 5.4e
1; Mismatches
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                                                                             Foran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNARE-dependent exocytosis;
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                                                                             PG;
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RESULT 12
AAU00257
ID AAU00
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AC AAU00
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DT 12-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC method of treating a patient suffering from poisoning or at risk of CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) CC to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of treating a patient in need of inhibition of SNARE-dependent exocytosis comprises CC from a cell capable of performing SNARE-dependent exocytosis comprises CC supplying a fragment, variant, fusion or derivative of a SNARE or an CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is useful in the manufacture of a medicament for the treatment of a patient CC suffering from poisoning or at risk of poisoning by clostridial toxin, CC e.g. from botulism or tetanus. The fragment, variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a recombinant CC entrynucleotide encoding the SNARE of the manufacture of medicament for the treatment of a patient CC polynucleotide encoding either of these SNARE polypeptides are useful in CC entry of SNARE-dependent exocytosis from a cell capable of creatment is satient out of critical state.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          taking the patient out of critical state. Note: The present sequence is not shown in the specification but derived from the mouse SNAP-25 sequence given in figure 8 (see M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents the amino acid sequence of synaptosomal-associated protein, SNAP25, mutant Q197K/R198K, used in a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating a patient suffering from poisoning or at risk of poisoning a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE -
                  12-SEP-2001
                                                     AAU00257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page - ; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dolly JO,
                                                                                      AAU00257
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                                                                                                                                                                                                                                                                                                                                                                                                    MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
                                                                                      standard;
                                                                                                                                                                            IMEKADSNKTRIDEANKKATKMLGSG
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                                                                                                                                                                                                                                              VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR
                                                                                                                                                                                                                                                                VDEREQMAISGGFIRRYTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR
                                                                                                                                                                                                                                                                                                                                                                                     O'Sullivan GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1041; Di
Pred. No. 3.5e
2; Mismatches
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Matches

Similarity

99 .0%;

Score 1039; Pred. No. 5 Mismatches

ນ.4e-90; 1;

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Conservative

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60 60 Sequence

206

AA;

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The present

the patient out of critical state. The present sequence is not shown in from the mouse SNAP-25 sequence g

in the sp given in

specification but in figure 8 (see A/

(see AAU00246).

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useful in the manufacture of a medicament for the treatment of a patie suffering from poisoning or at risk of poisoning by clostridial toxin, e.g. from botulism or tetanus. The fragment, variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding either of these SNARE polypeptides are useful the manufacture of medicament for the treatment of a patient in need of inhibition of SNARE-dependent exceytosis from a cell capable of performing SNARE-dependent exceytosis. The method of treatment is relatively fast, thus alleviating the symptoms when most severe and taking the patient out of control states.
                                                                                                                                                                                                                                                                                                                                              method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble (N-ethylmalelmide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE). The protein can be used in a method of toxin (toxin-inhibitory SNARE). The protein can be used in a method of treating a patient in need of inhibition SNARE-dependent exocytosis
                                                                                                                                                                                                                                                                     from a cell capable of performing SNARE-dependent exocytosis, comprises supplying a fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin resistant or tox inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE; toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis; synaptosomal-associated protein; mouse; mutant; mutein; N-ethylmaleimide-sensitive fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associated protein, SNAP25, mutant Q197A/R198K, used in a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents the amino acid sequence of synaptosomal-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page - ; 131pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSF-attachment protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Sullivan GA,
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RESULT 10
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Matches 205
The sequence represents the amino acid sequence of synaptosomal-associated protein, SNAP25, mutant M202A, used in a new method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)
                                                                                                                                               Example 1;
                                                                                                                                                                                       Treating a patient suffering from poisoning or at risk of poisoning a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE -
                                                                                                                                                                                                                                                                                                                                Dolly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxin-inhibitory SNARE; botulism; tetanus; synaptosomal-associated protein; mouse; mu N-ethylmaleimide-sensitive fusion protein;
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205; Conserv
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                                                                                                                                             Page - ; 131pp;
                                                                                                                                                                                                                                                                                                                              O'Sullivan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clostridial toxin; SNARE; toxin-resistant SNARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%;
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                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                              Mohammed N,
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Pred.
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No. 2
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                                                                                                                                                                                                                                                                                                                              Foran PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8e-90;
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Note: The present sequence is not shown in the specification but is derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).
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                           15-MAR-2001
                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                toxin-inhibitory SNARE; botulism; tetanus; SNARi
synaptosomal-associated protein; mouse; mutant;
N-ethylmaleimide-sensitive fusion protein;
soluble NSF-attachment protein receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE; toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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                                                                                                                                       "Wild-type
                                                                                                                                                                                                "Wild-type Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein,
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Pred. No. 2.8e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ed. No. 2.86
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNAP25, mutant Q197K/R198K.
                                                                                                                                          Arg
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                                                                                                                                          bу
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exocytosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in the manufacture of a medicament for the treatment of a patient suffering from poisoning or at risk of poisoning by clostridial toxin, e.g. from botulism or tetanus. The fragment, variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding either of these SNARE polypeptides are useful in the manufacture of medicament for the treatment of a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. The method of treatment is relatively fast, thus alleviating the symptoms when most severe and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated protein, SNAP25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents the amino acid sequence of synaptosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page - ; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolly JO, O'Sullivan GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-AUG-2000; 2000WO-GB03196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200118038-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-ethylmaleimide-sensitive fusion protein; soluble NSF-attachment protein receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reating a patient suffering from poisoning or at risk of poisoning clostridial toxin, e.g. botulism, comprises administering a
                                                                                                                                                                                                                                                                                                                                                      205;
                                                                                                                    61
                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is not shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the patient out of critical state
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQTDR
                                                                                                                 MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
                                                          VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR
                                                                                                                                                                                                                                     MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AA;
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the mouse SNAP-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9908-0149993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or toxin-inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                           99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mohammed N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutant Q197A, used in a
                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                           Score 1042; DB 22
Pred. No. 2.8e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence given in
                                                                                                                                                                                                                                                                                                                                                   Mismatches
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SNARE -
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                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a patient suffering from poisoning or a clostridial toxin, e.g. botulism, comprises toxin-resistant or toxin-inhibitory SNARE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-226739/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dolly JO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU00261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200118038-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-ethylmaleimide-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synaptosomal-associated protein, SNAP25, mutant R198A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMCO-) IMPERIAL COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synaptosomal-associated protein; mouse; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coxin-inhibitory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSF-attachment protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMEKADSNKTRIDEANARATKMLGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Wild-type Arg substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clostridial toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GA, Mohammed N, Foran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    botulism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNARE; toxin-resistant SNARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNARE-dependent exocytosis;
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Example 1; Page - ; 131pp; English

method of treating a patient suffering from poisoning or at risk of CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) CC to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of CC treating a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. CC supplying a fragment, variant, fusion or derivative of a SNARE or an CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is CC useful in the manufacture of a medicament for the treatment of a patient CC suffering from poisoning or at risk of poisoning by clostridial toxin, CC e.g. from botulism or tetanus. The fragment, variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a recombinant taking L.. polynucleotide encoding either of these SNARE polypeptides are useful in the manufacture of medicament for the treatment of a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. The method of treatment is associated protein, SNAP25, mutant R198A used in a The sequence represents the amino acid sequence of synaptosomal. the patient out of critical state fast, thus alleviating the symptoms when 'n specification new

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RESULT 7
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CC Note: The present sequence is not shown in the specification but is considered from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                               Key
Misc-difference
                                                                                                                                                                                                                                                                        toxin-inhibitory SNARE; botulism; tetanus; SNARE synaptosomal-associated protein; mouse; mutant; N-ethylmalelmide-sensitive fusion protein;
                                                          18-AUG-2000;
                                20-AUG-1999;
                                                                                           15-MAR-2001
                                                                                                                          WO200118038-A2
                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                     Mus
                                                                                                                                                                                                                                                                  soluble
                                                                                                                                                                                                                                                                                                             SNAP-25; poisoning; clo
toxin-inhibitory SNARE;
                                                                                                                                                                                                                                                                                                                             SNAP-25;
                                                                                                                                                                                                                                                                                                                                                         Synaptosomal-associated protein, SNAP25, mutant R198T.
                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         AAU00259;
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IMPERIAL COLLEGE INNOVATIONS LTD
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                                                                                                                                                                                                                                                                NSF-attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV
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                                                             2000WO-GB03196
                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑĄ;
                                99US-0149993
                                                                                                                                                                       198
                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                          clostridial toxin; SNARE; toxin-resistant SNARE;
aRE; botulism; tetanus; SNARE-dependent exocytosis;
                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.5%;
                                                                                                                                                    "Wild-type Arg
                                                                                                                                                                                                                                                                protein receptor
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Pred. No. 2.3e-90;
D; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
                                                                                                                                                    substituted
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                                                                                                                                                                                                                                                                                               mutein;
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RESULT 8
AAU00260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC The sequence represents the amino acid sequence of synaptosomal-
CC associated protein, SNAP55, mutant R1987 used in a new
CC associated protein, SNAP55, mutant R1987 used in a new
CC method of treating a patient suffering from poisoning or at risk of
CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)
CC to a cell of the patient, where the SNARE is resistant to proteolysis by
CC treating a patient sNARE) and/or is capable of inhibiting the
CC treating a patient, where the SNARE is resistant to proteolysis by
CC treating a patient, where the SNARE is capable of inhibiting the
CC treating a patient, where the SNARE is capable of inhibiting the
CC treating a fragment, variant, fusion or derivative of a SNARE or an
CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
CC useful in the manufacture of a medicament for the treatment of a patient
CC useful in the manufacture of a risk of poisoning by clostridial toxin,
CC e.g. from botulism or tetanus. The fragment, variant, fusion or
CC derivative of a SNARE or of an inhibitory SNARE polypetides are useful in
CC the manufacture of medicament for the treatment of a patient in need of
CC the manufacture of medicament for the treatment of apatient in need of
CC the manufacture of medicament for the treatment of apatient in need of
CC treatived from the supplement state.

CC relatively fast, thus alleviating the symptoms when most severe and
CC relatively fast, thus alleviating the symptoms when most severe and
CC user of the mouse SNAP-25 sequence given in figure 8 (see AAU00246).

CXX
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Best Local S
Matches 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating a patient suffering from po
a clostridial toxin, e.g. botulism,
toxin-resistant or toxin-inhibitory
SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosi
synaptosomal-associated protein; mouse; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1;
                                                                                 Synaptosomal-associated protein, SNAP25, mutant Q197A.
                                                                                                                          12-SEP-2001
                                                                                                                                                                                                      AAU00260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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205; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV 120
                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                          IMEKADSNKTRIDEANQRATKMLGSG
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                                                                                                                                                                                                                                                                                                                                                                                   VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR
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                                                                                                                                                                                                    Protein;
                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1042; DB 22
Pred. No. 2.8e-90;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             poisoning or at risk of poisoning n, comprises administering a ry SNARE -
                                                                                                                                                                                                                                                                                                                                          206
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                          exocytosis;
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RESULT 5
AAU00253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H
                                                                                                                                                                                                                                              The sequence represents the amino acid sequence of SNARE homologue, synaptosomal-associated membrane protein, hSNAP25b, used during analysis of SNAP-25. SNAP-25 mutants were used in a new method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can be used in a method of treating a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis from a cell capable to the cell of the patient. The toxin resistant or toxin inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant columns of the capable of a snake or an inhibitory SNARE or a recombinant columns.
                                                                                                         recombinant polynucleotide encoding the SNARE is useful in the manufacture of a medicament for the treatment of a patient suffering from poisoning or at risk of poisoning by clostridial toxin, e.g. from botulism or tetanus. The fragment, variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding either of these SNARE polypeptides are useful in the manufacture of medicament for the treatment of a patient in need of inhibition of SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           toxin-inhibitory SNARE; botulism; tetanus; SNARE-synaptosomal-associated protein; hSNAP25b; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating a patient suffering from poisoning or at risk of poisoning a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNAP-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNARE homologue, synaptosomal-associated protein, hSNAP25b
                                                                        dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. The method of treatment is relatively fast, thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 8; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-226739/23.
N-PSDB; AAS00370.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocvtosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2001
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                                                     alleviating the symptoms when most severe and taking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                       the
                                                     patient out
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Sequence

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RESULT 6
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                                       \begin{array}{c} \texttt{CCCCCC} \\ \texttt{CCCCC} \\ \texttt{X} \\
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Best Local :
associated protein, SNAP25, mutant L2U3A, useu in associated protein, SNAP25, mutant L2U3A, useu in associated protein, SNAP25, mutant E2U3A, useu in method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble poisoning by a clostridial toxin, comprising supplying a SNARE (soluble (N-ethylmanleimide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can be used in a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a patient suffering from poisoning or at risk of poisoning a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dolly JO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           toxin-inhibitory SNARE; botulism; tetanus; SNARI synaptosomal-associated protein; mouse; mutant; N-ethylmaleimide-sensitive fusion protein; soluble NSF-attachment protein receptor.
                                                                                                                                                                                                                                                                               The sequence represents the amino acid sequence of synaptosomal-
associated protein, SNAP25, mutant L203A, used in a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page - ; 131pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-AUG-2000; 2000WO-GB03196
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Pred. No. 7.6e-91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This amino acid sequence represents the mouse synaptosomal-associated protein of 25 kD (SNAP-25). The invention relates to a method for identifying a compound capable of affecting the binding of a syntaxin-binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-seci or VAMP, to syntaxin. The method comprises measuring the effect of the test compound on the extent of binding between the SBP and the SBP-binding site on syntaxin. The method can be used for identifying drugs capable of inhibiting or stimulating neurotransmitter release at the active zones of presynaptic membranes, which may be useful for treating CNS disorders affective or psychotic disorders, neurodegenerative diseases, hormonal or
SNAP-25; poisoning; clostridial toxin; SNAF toxin-inhibitory SNARE; botulism; tetanus;
                                                                                                                                 AAU00246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening assay for modulators of syntaxin binding - using comprising binding site of syntaxin, for identifying drugs for treating CNS disorders, neuro-degenerative diseases, et
                SNAP-25;
                                          Synaptosomal-associated protein,
                                                                         12-SEP-2001
                                                                                                      AAU00246;
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                                                                                                                                 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                             MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
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                                                                        (first entry)
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                                                                                                                                 Protein;
                clostridial toxin; SNARE; toxin-resistant SNARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                 206
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Pred. No. 7.6
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                                             SNAP25
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.6e-91;
 SNARE-dependent exocytosis;
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EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV

120

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cc associated protein, SNAP25. The sequence was used to create SNAP-25 double/single point mutants and C-terminal deletion cm trants used in a new method of treating a patient suffering from cc mutants used in a new method of treating a patient suffering from cc poisoning or at risk of poisoning by a clostridial toxin, comprising cc supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein) - cc attachment protein receptor) to a cell of the patient, where the SNARE is cresistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can be used in a method of treating a patient in need of inhibition of SNARE-cc dependent exocytosis from a cell capable of performing SNARE-dependent cexocytosis, comprises supplying a fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is useful in the manufacture of a medicament for the cell control of the snare for the cell of the patient, fusion or derivative of a SNARE or a trisk of poisoning content of a patient suffering from poisoning or at risk of poisoning contents. The strangment, fusion or derivative of a SNARE or of an inhibitory SNARE, or a snare content of a SNARE or of an inhibitory SNARE, or a SNARE or of an inhibitory SNARE, or a SNARE or of an inhibitory SNARE, or a snare content of a SNARE or of an inhibitory SNARE, or a snare content of a snare or of an inhibitory SNARE, or a snare content of a snare or of an inhibitory SNARE, or a snare or of an inhibitory SNARE, or a snare or of an inhibitory SNARE, or a snare or of an inhibitory SNARE.
                                                                                                                                                             Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                              recombinant polynucleotide encoding either of these SNARE polypeptides are useful in the manufacture of medicament for the treatment of a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. The method of treatment is relatively fast, thus alleviating the symptoms when most severe and taking the patient out of critical state.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating a patient suffering from poisoning or at risk of poisoning a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus
                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 8; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226739/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMCO.) IMPERIAL COLLEGE INNOVATIONS LTD
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                                                                                                                                                                                             Similarity
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                                        MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
MAEDADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
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                                                                                                                                                                                                                                                                                                              206
                                                                                                                                                             Conservative
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                                                                                                                                                                                     Score 1048; DB 22;
Pred. No. 7.6e-91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human 25 kD synaptosomal associated protein CC (SNAP-25), which is an inhibitory agent of the invention. The agents of the invention inhibit secretion of neurotransmitter from neuronal cells can dis an excitation-secretory uncoupling peptide (I) of at least 20 cc amino acids (aa) all of which correspond substantially to any one of CC amino acids (aa) all of which correspond substantially to any one of CC amino acids (aa) all of which correspond substantially to any one of CC atecholamine secretion from bovine chromaffin cells at a concentration co of 10 microM, especially 0.25 microM, or less. (I) are used, as a CC replacement for clostridium toxin, to inhibit release of CC neurotransmitters from synaptic vesicles, specifically for reducing CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering the drug to CC intracellular distribution of (I). Compounds for delivering the drug to CC intracellular for induction of apoptosis. Unlike the neurotoxins, (I) are not toxic or immunogenic and are more readily available. Their characterists for several days or weeks, so lower doses or less frequent treatments for several days or weeks, so lower doses or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 206
                                                                                                                                                                                 Hrs-2 polypeptide; ATP-preferring nucleotidase; SNAP-25; vesicle docking; calcium-regulated secretion; secretory vesicle; secretory process; brain; neurotransmitter release; presynaptic membrane; CNS disorder; depression; Parkinson's disease; endocrine system; hormonal imbalance; cell division; thought disorder; schizophrenia; degenerative disorder; anaesthesia; rat; immune system; antigen processing; immunomodulator; viral processing; central nervous system; vesicular release; affective disorder; human; anti-tumour application; membrane trafficking regulation; mouse.
                        26-FEB-1998;
                                                               03-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuro:transmitter release - used particularly for treating muscle spasticity, and for delivering drugs specifically to neural cells
                                                                                                       WO9838210-A2
                                                                                                                                                                                                                                                                                                                                                                            Mouse SNAP-25 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                        98WO-US03789
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RESULT 3
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Bin

AAW43426; 27-APR-1998

(first

entry)

AAW43426 standard;

Protein;

A

Binding domain;

mouse;

syntaxin; synaptosomal-associated

protein; CNS;

Mouse synaptosomal-associated protein-25

Qy Oy

VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR

180

VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR

EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV

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                                                                                                                                                                            This represents a mouse SNAP-25 polypeptide, a component of the protein CC polypeptides thought to underlie vesicle docking and fusion. The CC invention provides rat and human Hrs-2 polypeptides which are ATP-CC preferring nucleotidase that associate with SNAP-25. For identifying a CC compound capable of modulating calcium-regulated secretion of secretory CC vesicles, a SNAP-25 polypeptide can be contacted with a Hrs-2 CC polypeptide, in the presence and absence of a test compound. The effect CC if the test compound on the extent of binding between the SNAP-25 and CC Hrs-2 polypeptides are measured and a compound is identified as effective CC if its measured effect on the extent of binding is above a threshold CC level. The products can be used for identifying drugs capable of CC affecting secretory processes, such as neurotransmitter release at the CC active zones of presynaptic membranes. Such drugs can be used for CC treating disorders or conditions of the central nervous system by CC selectively enhancing or inhibiting vesicular release in specific areas CC of the brain, including affective disorders (e.g. depression), disorders CC intervention in antigen processing, as such as anaesthesia. The drugs can CC system for treatment of hormonal imbalances, the immune system for CC intervention in antigen processing, secreted immunomodulators, and vital processing, as well as anti-tumour applications, such as regulation of CC membrane trafficking during rapid cell division.
                                                             Matches 206;
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Pages 42-44; 55pp; English.
                                                                                                                                               Sequence
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ALIGNMENTS

RESULT 1 AAW30103 ID AAW3

AAW30103 standard; peptide;

206

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06-APR-1998

(first entry)

AAW30103;

synaptosomal associated protein; SNAP-25. Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; Excitation-secretory uncoupling peptide(s) for inhibiting WPI; 1997-479986/44. Montal M; WO9734620-A1. Synaptosomal associated protein. (REGC) UNIV CALIFORNIA 18-MAR-1996; 18-MAR-1997; 25-SEP-1997 Homo sapiens 96US-0013599 97WO-US04393

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Gapop 10.0 , Gapext 0.5
  September 16, 2003, 19:21:56; Search time 4.41558 Seconds (without alignments) 370.249 Million cell updates/sec
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	ore 83; DB : ed. No. 6.8e: Mismatches	n SNAP; ; PMID /EMBL/I	ep-19		; DB . 6.8e	3	10602, 1993 in SNAP-25 in t 8; PMID:8248151	3-Sep-199	ALIGNMENTS				
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R;Bark, I.C.; Wilson, M.C. Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I67823
A;Accession: I67823
                                                                                                                                                                              nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change
C;Accession: I67823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
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C:Species: Gallus gallus (chicken)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
                                               A; Molecule type: mRNA
A; Residues: 1-206 <RE:
A; Cross-references: Gl
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Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein
A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Accession: A37861
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A;Map position: 20p11.2-20p11.2
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llarity 100.0%;
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                                               GB:L19761; NID:g307427; PIDN:AAC37546.1;
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Pred. No. 6.9e-07;
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Pred. No. 6.9e-07;
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                                               PID:g307428
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О
SNARE protein 23 - mouse
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C:Accession: JC5512
R;Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, Biophys. Res. Commun. 234, 257-262, 1997
A:Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Muncl8c.
A:Reference number: JC5512; MUID:97312558; PMID:9168999
A;Accession: JC5512
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A; Residues: 1-210 < RI;
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A; Residues: 1-206 <OYL>
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13; Conserv
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17; Conserv
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17; Conser
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R;Risinger, C.; Blomqv1st, A..., 1993
J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of synaptosome-associated
A: Pafarence number: A49513; MUID:94043281; PMID:8226991
                                                                                                                                                                                                                                                                                                                                                                    synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiOyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E. J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, diff A;Reference number: A33623; MUID:90078337; PMID:2592413
A;Accession: A33623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C;Accession: A33623
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A;Map position: 20p11.2-20p11.2
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                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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NKARIDEANKHATKML
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Pred. No. 6.9e-07;
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Pred. No. 6.9e-07;
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Vesicle-membrane fusion protein SNAP-23A - human
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
C:Accession: JC5296
R:Mollinedo, F.: Lazo, P.A.
Blochem. Blophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion prote
A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5296
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-211 <MOL>
A;Cross-references: GB:Y09567; NID:g1924941; PIDN:CAA70760.1; PID:e290695; E
A;Cross-references: GB:Y09567; NID:g1924941; PIDN:CAA70760.1; PID:e290695; E
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C;Dete: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change
C;Accession: JC5297
R;Mollinedo, F; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane
A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5297
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
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hypothetical protein ZC8.4 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 C;Accession: T29999
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A;Residues: 1-210 <ARA>
A;Cross-references: DDBJ:AB000822; NID:g2189950; PIDN:BAA20345.1; PID:d1021177; PID:g218
C;Comment: This protein is involved in the insulin-induced translocation of vesicles con
                                                                              T29999
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9; Conservative
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                   #sequence_revision 15-Oct-1999 #text_change
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52.98;
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58.8%;
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Pred. No.
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A;Molecule type: DNA
A;Residues: 1-83 <DUC>
A;Residues: 1-83 <DUC>
A;Cross-references: GB.M25761; NID:g151334; PIDN:AAA25880.1; PID:g151335
A;Cornelis, P.; Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaert, V.;
Mol. Microbiol. 3, 421-428, 1989
A;Title: Cloning and analysis of the gene for the major outer membrane lipoprotein
A;Reference number: S04834; MUID:89313294; PMID:2473376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Y22F5A.3 - Caenorhabditis elegans (;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C;Accession: T26553 R;Gardner, A: submitted to the EMBL Data Library, January 1998 A;Reference number: Z20231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning, A;Reference number: A33854; MUID:89327122; PMID:2502533
A;Accession: A33854
                                                                                                                                                                                                                                                                                 outer membrane lipoprotein I precursor - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 31-Dec-2000 C;Accession: A33854; S04834; A44834; A83288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AL021479;
A;Experimental source: clone Y22F5A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid
A;Reference number: 20719
A;Accession: T2999
A;Status: preliminary; translated from GB/EMBL/DE
                                                                                                                                                                                                                                            R;Duchene, M.; Barron, C.; Schweizer, A.; von Specht, J. Bacteriol. 171, 4130-4137, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position:
A; Introns: 51/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-234 <WIL>
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                                                                                                                                                              A; Status: preliminary
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Best Local :
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7; Conserve
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41.2%; Pred.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAA16322.1; GSPDB:GN00023; CESP:Y22F5A.3
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transmembrane transport protein Cj0182 [imported] - Campylobacter jejuni (strain N C;Species: Campylobacter jejuni C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C;Accession: E81436 R;Parkhill, J: Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Nature 403, 665-668, 2000
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                                                                                                                                                                                                          A;Gene: Cj0182
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: sequence extracted from NCBI backbone (NCBIN:103666, NCBIP:103667)
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathology. R; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X13748; NID:g45344; PIDN:CAA32013.1; PID:g45345 A;Note: the authors translated the codon GAA for residue 78 as Gly R;Saint-Onge, A.; Romeyer, F.; Lebel, P.; Masson, L.; Brousseau, R. J. Gen. Microbiol. 138, 733-741, 1992
A;Title: Specificity of the Pseudomonas aeruginosa PAO1 lipoprotein I gene A;Reference number: A44834; MUID:92268853; PMID:1588307
A;Status: preliminary
밁
                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72665.1; PID:g696767
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-401 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype; A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: E81436
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-83/Product: lipoprotein I #status predicted <MAT>
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A;Residues: 1-83 <SAI>
A;Cross-references: GB:X58714; GB:S36066; NID:g433509; PIDN:CAA41550.1; PID:g433510
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A;Experimental source: strain PAO1
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A; Residues: 1-83 <STO>
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A; Residues: 1-83 <COR>
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71 NNATLIQEANQRA 83
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DEANERALRML 77
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                                                                                                      Conservative
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72.7%;
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Pred. No. 18;
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                                                                                                      Mismatches
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RESULT 15

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C; Accession: Sous
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submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae lambda
A;Reference number: S50427
A;Accession: S50562
Search completed: September 16, Job time: 5.41558 secs
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                                                                                                                                                                                                        A;Cross-references: SGD:S0000861; MIPS:YER059w A;Map position: 5R
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                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein YER059w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 10-May-2001
                                                                                                                                                                                                                                            A; Gene: SGD: PCL6
                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-420 <DIE>
                                                                                                                                        Matches
                                                                                                                                                         Query Match
Best Local
                                                                   283 SNESSLDKANRGADKM
                                                                                                                                      Similarity
8; Conserv
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                                                                                                    SNKTRIDEANQRATKM 16
                                                                                                                                      Conservative
                                                                                                                                                       50.6%;
                                                                   298
                2003, 19:30:48
                                                                                                                                                         Score 42; DE
Pred. No. 19;
                                                                                                                                        Mismatches
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                                                                                                                                                                       Length 420
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
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Match
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1048
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Gapop 10.0 ,
   95.8
90.8
80.3
86.5
67.1
67.1
60.9
60.9
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sp_bacteria:*
sp_fungi:*
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sp_bacteriap:*
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sp_rodent:*
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sp_mammal:*
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Q8axm1 xenopus lae
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Interpro; IPR000727; T_SNARE.
Pfam; PF00035; SNAP-25; 1.
SMART; SW00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 206 AA; 23336 MW;
                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to synaptosomal-associated protein, 25kD.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC010647; AAH10647.1; -.
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121 VDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR
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                                                                                               EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV 120
                                           EEGMNHT NQDMKEAEKNLKDLGKCCGLFTCPCNKLKSSDAYKKAWGNNQDGVVASQPARV
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Pred. No. 1.6e-61;
5; Mismatches 4;
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Matches 196
                                                                                             SEQUENCE FROM N.A. KOLK S.M., Groffen A.J.A., T Submitted (JAN-2001) to the EMBL; AF335586; AAO13788.1; SEQUENCE 206 AA; 23122 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

KOlk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubc Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF335587; AA013789.1; -.

SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;
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Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniai
Amphibia; Batrachia; Anura; Mesobatra
Xenopodinae; Xenopus.
                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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01-MAR-2003 (TrEMBLrel.
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NCBI_TaxID=8355;
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                                   Local Sim
nes 186;
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                                                                                                                                                                                                            Xenopus
                                                                                                 23122 MW;
                                              90.8%;
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                                                                                                                             Tuinhof R., Verhage M., Roub
e EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                           Created)
Last sequence
Last annotation
                              Score 952; DB Pred. No. 5.8e 8; Mismatches
                                                                                                                                                                                                                             a; Craniata; Vertebrata; |
Mesobatrachia; Pipoidea;
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Pred. No. 1.6e
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01-NOV-1998 (TrEMBLrel. 0
01-OCT-2002 (TrEMBLrel. 2:
SYNAPTOSOME-ASSOCIAted pro
25,2).
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EMBL; AF091594; AAC64290.1; -.
EMBL; AF091596; AAC73007.1; -.
ZFIN; ZDB-GENE-980526-392; snapp2
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF000835; SNAP-25; 1.
SWART; SM00397; T_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 203 AA; 22647 MW; 9
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Eukaryota; Metazoa; Chordata; I
Actinopterygii; Tv
Cyprinidae; Danio.
NCBI_TaxID=7955;
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093579;
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                                                                                               IMEKADSNKTRIDEANQRATKMLGSG
                                                                                                                                                VDEREQMAISGGFIRRVTNDARENEMDENLEQVGSIIGNLXHMALDMGNEIDTQNRQIDR
                                                                                                                                                                                                               EEGMDQINKDMKEAEKNLTDLGNLCGLCPCPCNKLKGGG---QSWGNNQDGVVSSQPARV
                                                                                                                                                                                                                               EEGMDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARV
                                                                                                                                                                                                                                                                              MADESDMRNELNDMQARADQLGDESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERI
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                                                                              IMDMADSNKTRIDEANQRATKMLGSG
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                           88.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snap25b
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Last sequence update)
Last annotation update)
ein 25.2 (SYNAPTOSOME as
                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                                                                                                                                                                                                          Score 925.5;
Pred. No. 3.8e
8; Mismatches
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n; Craniata;
Teleostei;
 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                           93B7590DD0C93F38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein groups s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     suggests
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les 13;
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Best Local S
Matches 179
                                                                                                                                           P70557;

01-FEB-1997 (TrEMBLrel. 02, Crei
01-FEB-1997 (TrEMBLrel. 02, Lasi
01-CCT-2002 (TrEMBLrel. 22, Lasi
SNAP-25a (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; C
Mammalla; Eutheria; Rodentia; S
          Submitted (APR-1996) to the EMB
EMBL; U56261; AAA99825.1; -.
InterPro: IPR000928; SNAP-25.
InterPro: IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
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InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                            Madison D.L., Pfeiffer "SNARE proteins may be myelin membrane.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Madison D.L., Pfeiff
"SNARE proteins may
membrane.";
                                                                                                         TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
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01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                86.5%;
nilarity 98.4%;
Conservative
                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                            PRELIMINARY;
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ins may be
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20585 MW;
                                                                                      S.E.;
utilized
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utilized
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Last sequence
Last anno
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Last sequence up
                                                                   EMBL/GenBank/DDBJ databases
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Pred. No. 6.6e
1; Mismatches
                                                                                                                                              Craniata; Ver
Sciurognathi;
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                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                   sequence update)
annotation update)
                                                                                     oligodendrocytes
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                                                                                                                                               Vertebrata;
thi; Muridae;
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on update)
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                                                                                      for
                                                                                                                                                         Euteleostomi;
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; Murinae; Rattus
                                                                                                                                               Murinae;
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Best Local S
Matches 172
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osada N., Hida M., Kusuda J., Tanuma R., Is
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from
libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DI
Submitted (OCT-2000) to the EMBL/GenBank/DI
EMBL; AB04985; BAB16738.1; -
InterPro; IPR000728; SNAP-25.
InterPro; IPR000727; T.SNARE.
Pfam; PF00835; SNAP-25; 1.
SNART; SM00397; T.SNARE; 1.
PROSITE: PS50192; T.SNARE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50
Hypothetical
SEQUENCE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 16.0 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9GM34;
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae;
NCBI_TaxID=9541;
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136; Conserv
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                                                                                                                                                                                                         REQMAISGGFIRRYTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIME
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                                                                                           KADSNKTRIDEANQRATKMLGSG
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                                                                                                                                        KADSNKTRIDEANQRATKMLGSG
                                                                                                                                                                                   REQMAISGGFIRRYTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             al protein.
143 AA; 1
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181 AA;
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                                                                                                                                                                                                                                                                                                                                                                     Conservative
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20558 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16043 MW;
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94.5%;
                                                                                                                                                                                                                                                                                                                                                                                        67.1%;
95.1%;
                                                                                                                                                                                                                                                                                                                                                                  ; Score 703; DB; Pred. No. 4.6e
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Pred. No. 2.3e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                D625DBAAA0893FB0
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.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iseki K.,
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novel SNAP-25 related

protein expressed

in many

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RAA WEEKERAA WEEKERAA
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C 009044;
C 009044;
T 01-JUL-1997 (TrEMBLrel. 04, Created)
JT 01-JUL-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-CTT-2002 (TrEMBLrel. 22, Last annotation update)
E SYNDET (SNAP-23) (Synaptosomal-associated protein, 23K-23 OR SNDT.
SNAP23 OR SNDT.
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Best Local s
Matches 128
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InterPro; IPR000928; SNAP-25.
InterPro; IPR0009727; T_SNARE.
Pfam; PP00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS501192; T_SNARE; 2.
SEQUENCE 210 AA; 23235 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116; [1]
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070377;
01-AUG-1998
01-AUG-1998
01-OCT-2002
Wang G.,
Baldini
                                                                                                MEDLINE=97312558; PubMed=9168999; Araki S., Tamori Y., Kawanishi M., Shinoda H., Mas Araki S., Tamori Y., Kawanishi M., Shinoda H., Mas Niki T., Okazawa H., Kubota T., Kasuga M.; "Inhibition of the binding of SNAP-23 to syntaxin Biochem. Biophys. Res. Commun. 234:257-262(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99162237; PubMed=10051443;
MEDLINE=99162237; Cabaniols J.P., Cus
                   MEDLINE=97220227; Publ
Wang G., Witkin J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. J. 338:709-715(1999).
EMBL; AF052596; AAC06031.1; -.
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                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=10090
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  i G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEAEKNLTDLGKFCGLCVCPCNKLKSSDA---YKKAWGNNQD----GVVASQPARVVDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEKADTNKNRIDIANTRAKKLIDS
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3 (TrEMBLrel.
2 (TrEMBLrel.
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                                            PubMed=9067602;
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Rodentia;
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22,
                      G.,
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Last sequence update)
Last annotation update)
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Pred.
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                      Bankaitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cushman S.W., Roche P.A.; complex assembly in rat adipose
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No. 5
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                   V.A.,
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.7e-37;
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                      Scherer
                                                                                                                                                                     Masugi J.,
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; Murinae; Mus
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RC MEDLINE-C37BL/G; TISSUE-Embryo;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Baldarelli R., Barsh G.,
RA Shrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Nordone P., Ring B., Ringwald M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hyasahtaki Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                    EMBL; ...
EMBL; AKOlya.

EMBL; AKOlya.

MGD; MGI:109356; ...

InterPro; IPR000928; Sa...

InterPro; IPR000727; T_SNARE.

Pfam; PF00835; SNAP-25; 1.

Pfam; PF00835; SNAP-25; 2.

"". SM00397; L_SNARE; 2.

"". SM00397; L_SNARE; 2.

"". 23261 MW; f
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
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EMBL; AB000822; BAA20345:1; -.

EMBL; AF213257; AAF23503:1; -.

EMBL; AF213257; AAF23503:1; JOINED.

EMBL; AF213251; AAF23503:1; JOINED.

EMBL; AF213253; AAF23503:1; JOINED.

EMBL; AF213254; AAF23503:1; JOINED.

EMBL; AF213254; AAF23503:1; JOINED.

EMBL; AF213256; AAF23503:1; JOINED.

EMBL; AF213256; AAF23503:1; JOINED.

EMBL; AF213256; BAA23507:1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
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187
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TEKADTNKNRIDIANTRAKKLIDS
                                     MEKADSNKTRIDEANQRATKMLGS
                                                                                                                                                                                                                                                           EEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKDM
                                                                           PQQTTGAASGGYIKRITNDAREDEMEENLTQVGSILGNLKNMALDMGNEIDAQNQQIQKI
                                                                                                                     EQM--
                                                                                                                                                             REAEKTLTELNKCCGLCICPCNRTKNFESGKNYKATWGDGGDNSPSNVVSKQPSRITNGQ
                                                                                                                                                                                                                                          EEVQLRAHQVTDESLESTRRILGLAIESQDAGIKTITMLDEQGEQLNRIEEGMDQINKDM
                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110:505-513(1997).
                                                                                                  -AISGGFIRRYTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRI
                                                                                                                                                                                                                                                                                                                                             61.6%;
62.3%;
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                                                                                                                                                                                                                                                                                                                                             Score 646;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                       6919E127E16BA2C9 CRC64;
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                                       205
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RESULT

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O35620
ID O35620;
AC O35620;
DT O1-JAN-1998 (TrEMBLrel. 05, Created)
DT O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT O1-JAN-1998 (TrEMBLrel. 22, Last annotation update)
DT O1-JAN-1998 (JAST Craniata; Vertebrata; Eutoral Craniata; Eutoral Craniata; Vertebrata; Eutoral Crania
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Best Local S
Matches 126
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01-JUN-2001
01-OCT-2002
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
                                                                                                                                                       STRAIN=C57BL/6J; TISSUE-Head; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                       Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
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                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Synaptosomal-associated
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                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence up
(TrEMBLrel. 22, Last annotation
1-associated protein, 23kD.
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                                                                                                                                                                                                                                                                            (Mouse)
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Rodentia;
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Pred. No. 1.3e
32; Mismatches
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Sciurognathi; Muridae;
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1.3e-36;
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Murinae; Mus
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RESULT 12
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Best Local :
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Kolosova I.A., Timmers K., King
Submitted (APR-1998) to the EMI
EMBL; AF061750; AAC83577.1; -.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
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InterPro; IPR000727; T_SNARE.
Pfam; PF000835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 221 AA; 24550 MW;
                                                                                                                                                                                              TISSUE-Ovary;
MEDLINE-99057936; PubMed-9837952;
MEDLINE-99057936; PubMed-9837952;
Tahara M., Coorssen J.R., Timmers K., Black Stheller R., Zimmerberg J.;
Scheller R., Zimmerberg J.;
"Calcium can disrupt the SNARE protein concentration can disrupt the snare protein concentration concentration concentration concentration concentration concentration."

J. Biol. Chem. 273:33667-33673(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         076338 PRELIMINARY; PRT; 212 AA.
076338; O1-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Kordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Haveshiyaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ovarian synaptosome-associated protein 25 homolog.
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinocea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AKO17311; BAB30686.1; -.
MGD; MGI:109356; Snap23.
                                                                                                                                            TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7668;
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                                                                                                                                                                  SEQUENCE FROM
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                                                                                            Kingsley D.H., Bezrukov L., 'e EMBL/GenBank/DDBJ databases
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01-MAR-2003
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      044419
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Eumalacostraca; Eucarida
Astacoidea; Cambaridae;
NCBI_TaxID=6728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yasuda-Kamatani Y., Yasuda A.;
"Identification of synaptosome-associated protein the hepatopancreas and the brain of the crayfish,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Procambarus
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212 AA;
                                                                                                                                                                                                                                                                                                                                                                           AISGGFIRRVINDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADS
                                                                                                                                                                                                                                                                                                              NKDMKEAEKNITDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARVVDEREQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt MEDDRDGCGGNASMITRITNDAREDEMDENLTQVSGIVGNLRHMAIDMQSEIGAQNSQVG}
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                                                                                                                NTARVNMANERAGSLL
                                                                                                                                         NKTRIDEANQRATKML
                                                                                                                                                                                                    GASGGYIGRITNDAREDEMEDNMGQVNTMIGNLRNMAIDMGSEIENQNRQITRINAKAGS
                                                                                                                                                                                                                                                                                          NADMKEAEKNLTGMEKCCGLCVLPCNKSSQFKEDESTWKGKEDGVVSSQPQRVMDDRNGL
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Eucarida; Decapoda; Pleocyemata; Astacid
oaridae; Procambarus.
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62.3%;
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Matches
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Schulz J.R., Sasaki J.D., Vacquier V.D.;

"Increased association of synaptosome associated prowith syntaxin and vesicle-associated membrane prote:
acrosomal exocytosis of sea urchin sperm.";
J. Biol. Chem. 273:2435-24359(1998).

EMBL; AF036902; AAC35867.1;
Interpro; IPR000928; SNAP-25.
Interpro; IPR000928; SNAP-25.
Interpro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; I.
SMART; SM000397; T_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 212 AA; 24108 MW; 47C1EB69459F250A CRC
                                                                                                                                                                                                                                                                                                                                           O9VH76 PRELIMINARY;
O9VH76;
01-MAY-2000 (TIEMBLIEL 1
01-MAY-2000 (TIEMBLIEL 1
01-OCT-2002 (TIEMBLIEL 1
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01-JUN-1998 (TrEMBLrel. (
01-JUN-1998 (TrEMBLrel. (
01-OCT-2002 (TrEMBLrel. ;
Synaptosomal-associated)
SEQUENCE FROM N.A.

STRAIN-BERKELEY;

MEDLINE-20196006; PubMed-10731132;

MEDLINE-20196006; PubMed-10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson elegency R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos (Marchaell M.D.)
                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Haspoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                          CG9474 protein (SNAP-24 protein). SNAP24 OR SNAP-24 OR CG9474.
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Strongylocentrotus
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NCBI_TaxID=7668;
                                                                                                                                                                                                      NCBI_TaxID=7227;
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22, Last annotation
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Search completed: September 16, 2003, 19:29:41 Job time: 133.091 secs
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchar I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Davis N.J., Evangelista C.C., Ferrac C., Ferrac E., Wang A.H., Wang X.,
RA Malliams S.M., Woodser T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Klamel B.S., Kondina N.J., Weinsenbach J.,
RA Zheng X.H., Khong F.N., Zhong W., Zhong M., Shang A.H., Wang X.,
RA Shen B.C., Sagaran D.A., Weinsenbach J.,
RA Zheng X.H., Mondager T., Worley K.C., Wu D., Yang S., Yao Q.A.,
"The genome sequence of Drosophila melanogaster.";
RN L. Schence 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
SEQUENCE 212 AA; 23554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AE003684; AAF54443.1; -. EMBL; AF187106; AAF384.1; -. F1yBase; FBgn0028401; Snap24. InterPro; IPR000928; SNAP-25. InterPro; IPR000727; T_SNARE. DFGG. PRO00727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Niemeyer B.A., Schwarz T.L.;
"SNAP24, a Drosophila SNAP-25 homolog on granule membranes, is a
putative mediator of secretion and granule-granule fusion in salivary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glands.";
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                                                                                                                         IDRIMEKADSNKTRIDEANQRATKMLGS 205
                                                                                    VDRINAKGDANNIRMDGVNKRANNLLKS
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Result
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Maximum DB seq length: 2000000000
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52,	48,	56,	52,	e 48,	85,	85,	54,	49,	47,	e 31,	e 54,	e 49,	47,	31,	e 29,	29	e 55,	55	12	7,	2.	12	e 7,	e 2,	14	e 14,	e 11,	Sequence 38, App	
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ALIGNMENTS

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APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
ITILE OF INVENTION: Fret Protease Assays For Botulinum
ITILE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 17
ORGANISM: Homo Sapiens
US-09-942-024-30
Sequence 30, Application US/09942098
Publication No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/09942024 Publication No. US20030143650A1 GENERAL INFORMATION:
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17; Conserv
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Pred. No.
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Residues 187-203 of SNAP-25
US-10-011-588-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-09-942-098-30
                                                                        Sequence 32, Application US/09942024 Publication No. US20030143650A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 17
TYPE: PRT
                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PITITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY FILE REFERENCE: A34796 067252.0113
                                      APPLICANT: Steward, APPLICANT: Fernande
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/611,419
PRIOR FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: 60/246,744
PRIOR FILING DATE: 2000-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/910,186 PRIOR FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/011,588 CURRENT FILING DATE: 2002-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 17
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: P-AR 4802
                         PPLICANT:
       OF INVENTION:
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Fernandez-Salas, Ester
Aoki, Kei Roger
VENTION: Fret Protease Assays For Botulinum
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Pred. No.
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Pred. No. 7e-08;
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NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Ve
SEQ ID NO 89
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-32
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Matches
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SEQ ID NO 32
LENGTH: 18
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SEQ ID NO 32
LENGTH: 18
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                            TITLE OF INVENTION: Fret Protease Assays For Botulinum TITLE OF INVENTION: Serctype A/E Toxins FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEO, ID NOS: 96
                                                                                                                                                                                                                                                          APPLICANT: Steward, Lance E. APPLICANT: Fernandez-Salas, Ester APPLICANT: Aoki, Kei Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Fret Protease Assays For Clostridial TITLE OF INVENTION: Toxins FILE REFERENCE: P-AR 4802 CURRENT APPLICATION NUMBER: US/09/942,098 CURRENT FILING DATE: 2001-08-28 NUMBER OF SEQ ID NOS: 96
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CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Steward, APPLICANT: Fernand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Aoki, Kei Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: synthetic peptide NAME/KEY: MOD_RES
                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 17; Conserv
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                                                                                                                             for Windows Version 4.0
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Pred. No. 7.5
); Mismatches
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Pred. No. 7.5e-08;
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NAME/KEY: AMIDATION
LOCATION: (0)...(0)
OTHER INFORMATION: at the C-terminal
US-09-942-098-89
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CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 89
LENGTH: 21
TYPE: PRT
                                                                                                                                   Sequence 88, Application US/09942024 Publication No. US20030143650A1 GENERAL INFORMATION:
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Best Local :
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Best Local
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
                                TITLE OF INVENTION: Fret Protease Assays For Botulinum TITLE OF INVENTION: Serotype A/E Toxins FILE REFERENCE: P-AR 4803
                                                                             APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
CURRENT APPLICATION NUMBER: US/09/942,024
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OTHER INFORMATION: Xaa-fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 21
OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: synthetic peptide NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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LOCATION: 21
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17; Conserv
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No. US20030143651A1
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Pred. No.
                                                                                                                                                                                                                                                                                                                                              Score 83;
Pred. No.
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thes 0;
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NAME/KEY: AMIDATION
LOCATION: (0)...(0)
OTHER INFORMATION: 6
US-09-942-098-88
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US-09-942-098-88
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 88
LENGTH: 23
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 88
                                                              Matches
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Best Local
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Publication No.
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APPLICANT: Fernandez-Salas, Ester
APPLICANT: Fernandez-Salas, Ester
TITLE OF INVENTION: Fret Protease Assays For Clostridial
TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
                                                                                                                                                                                                     OTHER INFORMATION: NAME/KEY: MOD_RES LOCATION: 23
                                                                                                                                                                                                                                                  OTHER INFORMATION:
NAME/KEY: MOD_RES
LOCATION: 1
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LOCATION: (0)...(0)
OTHER INFORMATION: at the C-terminal
                                                                                                                                                                                       OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial
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OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
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NAME/KEY: MOD_RES
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NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                                                                                    FEATURE:
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                1 SNKTRIDEANQRATKML 17
                                                            Similarity
17; Conserv
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17; Conserva
SNKTRIDEANQRATKML 19
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                                                              Conservative
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Pred. No.
                                                                             Score 83;
Pred. No.
                                                              Mismatches
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hes 0;
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s 0;
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                                                                                          Length 23;
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                                                              Indels
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RESULT 10
US-09-942-024-90
; Sequence 90, Application US/09942024
; Publication No. US20030143650A1

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TITLE OF INVENTION: Toxins
FILE REFERENCE: P-AR 4802
CURRENT FAPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 90
LENGTH: 24
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Aoki, Kei Roger
ITITLE OF INVENTION: Fret Protease Assays For Botulinum
ITITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 90
LENGTH: 24
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                               US-09-942-098-90
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     Matches
                                        Query Match
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APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Steward, Lance E. APPLICANT: Fernandez-Salas,
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                                                                                         NAME/KEY: AMIDATION
LOCATION: (0)...(0)
OTHER INFORMATION: at the C-terminal
                                                                                                                                            OTHER INFORMATION: Xaa-fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 24
OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
                                                                                                                                                                                                                           OTHER INFORMATION:
NAME/KEY: MOD_RES
LOCATION: 1
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LOCATION: (0)...(0)
OTHER INFORMATION: at the C-terminal
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NAME/KEY: MOD_RES
LOCATION: 24
OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
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OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: 1
   Local Similarity 100 nes 17; Conservative
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nes 17; Conserv
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                 Score 83; DB 12
Pred. No. 1e-07;
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Pred. No.
   Mismatches
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                                    12;
 0;
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US-09-942-024-38
; Sequence 38, Application US/09942024
; Publication NO. US20030143650A1
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US-09-942-024-37
IS Sequence 37, Application US/09942024
Publication No. US20030143650A1
GENERAL INFORMATION:
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: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 33
: LENGTH: 33
: TYPE: PRT
: ORGANIZM: Mus musculus
US-09-942-024-33
                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Carassius US-09-942-024-37
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GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas,
APPLICANT: Aoki, Kei Roger
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 37
LENGTH: 33
TYPE: PRT
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fernandez-Salas, Ester
APPLICANT: AOK1, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/942,024 CURRENT FILING DATE: 2001-08-28
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 Fernandez-Salas,
Aoki, Kei Roger
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Pred. No. 1.5e-07;
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Pred. No. 1.5e-07;
Mismatches 0;
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: TITLE OF INVENTION: Fret Protease Assays For Botulinum
: TITLE OF INVENTION: Serctype A/E Toxins
: FILE REFERENCE: P-AR 4803
: CURRENT APPLICATION NUMBER: US/09/942,024
: CURRENT FILING DATE: 2001-08-28
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: FastSEQ for Windows Version 4.0
: SQF ID NO 38
: LENGTH: 33
: TYPE: PRT
: ORGANISM: Carassius auratus
US-09-942-024-38
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 33
TYPE: PRT
ORGANISM: Mus musculus
US-09-942-098-33
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-942-098-33
; Sequence 33, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
    APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
    APPLICANT: AOKL, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial;
    TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; FILE REFERENCE: P-AR 4802
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Search completed: September 16, 2003, 19:31:53 Job time: 4.41558 secs
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Maximum DB
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Listing first 45 summaries
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Human polypeptide
Human SNAP-25 N-te
Neurotransmitter s
Neurotransmitter s
Neurotransmitter s
SNAP-25 residues 1
Human SNAP-25 N-te
                                                                                                                                                                                                             Description
                                                                                                                                                Amino acids 187-20
Human SNAP25 (amin
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Synaptosomal-assoc	AAU00259	22	206		77	45
Synaptosomal-assoc	AAU02636	22.	203		77	44
Clostridial neurot	AA015166	23	116		77	43
3	AA015162	23	24		77	42
_	AAY44066	20	17		77	41
Human SNAP25 (amin	AAY44065	20	17		77	40
SNAP25	AAY44064	20	17		77	39
Human SNAP25 (amin	AAY44056	20	17		77	38
Human SNAP25 (amin	AAY44054	20	17		77	37
Human SNAP25 (amin	AAY44053	20	17		77	36
SNAP25	AAY44051	20	17		77	35
Human SNAP25 (amin	AAY44048	20	17		77	34
SNAP25 (AAY44046	20	17		77	ω ω
_	AAY44044	20	17		77	32
Human SNAP25 (amin	AAY44040	20	17		77	31
Human SNAP25 (amin	AAY44022	20	17		77	30
-	AAY44070	20	17		78	29
SNAP25	AAY44062	20	17		78	28
SNAP25 (AAY44049	20	17		78	27
SNAP25	AAY44045	20	17		78	26
	AAY44039	20	17		78	25
ģ	AAU02640	22	206		79	24
Human SNAP25 (amin	AAY44059	20	17		79	23
Human SNAP25 (amin	AAY44052	20	17		79	22
_	AAY44050	20	17	95.2	79	21
SNAP25	AAY44047	20	17		79	20
SNAP25	AAY44069	20	16		79	19
SNAP25	AAY44063	20	17		80	18
SNAP25 (ami	AAY44038	20	17		80	17
homologue,	AAU00253	22	206	100.0	83	16
SNARE homologue, s	AAU00252	22	206		83	15
ct	AAU00246	22	206		83	14
synaptos	AAW43426	19	206	•	83	13
U.	AAW79198	19	206	8	83	12
\vdash	AAW30103	18	206	0	83	11
Clostridial neurot	AA015165	23	116	100.0	83	10

ALIGNMENTS

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Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis; fluorescamine; detection; human; synaptosomal protein; SNAP25; hydrolysis; amino group.
        Quantitation of type A botulinum toxin
                       WPI; 1999-579939/49.
                                                                                   06-NOV-1996;
                                                                                                                  US5965699-A
                                                                                                                               Homo sapiens
                                                                                                                                                                                            18-JAN-2000
                                                                                                                                                                                                           AAY44021;
                                                                                                                                                                                                                         AAY44021 standard;
                                                    (USSA ) US
                                                                    06-NOV-1996;
                                                                                                  12-OCT-1999
                                                                                                                                                                             Amino acids 187-203 of human SNAP25
                                      ΚA,
                                                     SEC OF ARMY.
                                                                                                                                                                                           (first entry)
                                      Schmidt
                                                                    96US-0743894
                                                                                   96US-0743894
                                                                                                                                                                                                                         peptide;
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Best Local
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The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. Botulinum toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the peptide at different time points; and measuring the amount of hydrolysis at each time point by combining with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               botulinum neurotoxin type A using fluorescamine detection. The method comprises adding an analogue (e.g. AAY44022-Y44076) of this peptide (which represents amino acids 187-203 of the human synaptosomal protein SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the peptide at different time points; and measuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label represents with a label capable of detecting from the hydrolysis.
                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis; fluorescamine; detection; human; synaptosomal protein; SNAP25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an enzymatic assay for the quantitation o type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. The met
                                                                                                                                                                                   Disclosure; Column 9; 28pp;
                                                                                                                                                                                                                   Quantitation of type A botulinum toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydrolysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY44057;
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                                                                                                                                                                                                                                                                                                                    (USSA) US
                                                                                                                                                                                                                                                      1999-579939/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SNKTRIDEANQRATKML 17
                                                                                                                                                                                                                                                                                     KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       botulinum toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acids 187-203) analogue #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
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Best Local
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                                                          useful in vaccination against botulism, for eliciting protective immunity in a mammal, for treating dystonias, spasticity, pain, ocular motility, facial dyskinesias, stiff-person syndrome, bladder dysfunction, segmental myoclonus, hyperkinetic disorders, cosmetic treatment of facial wrinkles, conditions characterised by hyperactivity of the lower motor neuron, and to control autonomic nerve function or tiproe-walking due to stiff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botulinum neurotoxin light chain; BoNT LC; botulism; dystonia; pain; spasticity; ocular motility; facial dyskinesia; stiff-person syndrome; bladder dysfunction; segmental myoclonus; hyperkinetic disorder; human; cosmetic treatment; facial wrinkle; cerebral palsy; analgesic; relaxant; lower motor neuron hyperactivity; autonomic nerve function; muscular; lower motor neuron hyperactivity; autonomic nerve function; muscular;
          muscles common in children with cerebral palsy. The seque useful for screening for botulinum neurotoxin inhibitors. represents a human polypeptide C-terminal fragment, used
                                                                                                                                                             The invention relates to a nucleic acid molecule encoding a botulinum neurotoxin light chain (BONT LC) serortype A, where the DNA has a sequence that is expressible in a host organism other than Clostridium, or has a total A+T content that is less than about 70% The BONT LC protein is
                                                                                                                                                                                                                                                                                             Novel nucleic acid molecule encoding botulinum neurotoxin light serotype A, useful for producing the neurotoxin for vaccination botulism, comprises sequence expressible in host other than Clos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured under similar conditions. The method is useful for the quantitation of type A botulinum toxin.
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20-JUL-2001;
                                                                                                                                                                                                                                               Example
                                                                                                                                                                                                                                                                                                                                                                                                 Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                               (USSA) US
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17; Conserv
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                                                                                                                                                                                                                                               Page 62; 166pp; English.
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; 2001US-0910186.
; 2001US-311966P.
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                                               The sequences are also
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                                  This sequence
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RESULT 4
AABJUST86
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RESULT 5
AAW30100
ID AAW3
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Best Local S
Matches 17
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                                                                                                                                                                                                                                                      The invention relates to new peptides comprising 3-30 contiguous amino acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated protein 25). The peptides AAB15581-B15586 represent examples of the peptides of the invention. The peptides have neuronal exocytosis inhibitory activity and are used for treatment of factal wrinkles and asymmetry and pathological neuronal exocytosis-mediated pathological disorders and alterations manifested e.g. by spasms and neurological and neurodegenerative disorders.
AAW30100 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dermatological; neuroprotective; SNAP-25; synaptosomal-associated neurodegenerative disorder.
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fernandez Ballester
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                                                                                                                                                                                                                                                                                                                                                                                                                  17; Page 34; 40pp; Spanish.
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                                                                                                        SNKTRIDEANQRATKML 17
                                                                                      SNKTRIDEANQRATKML 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing amino acid : neurological disorders
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ter GJ, Planell Cases R
, Gutierrez Perez LM,
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100.0%; Pr
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Pred. No. 1.3
); Mismatches
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Pred. No. 1.1e-07;
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protein 25; facial wrinkle; asymmetry;
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Carbonell Castell T;
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RESULT 6
AAW30099
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                                                                                                                                                                                                                                                                                                                                  AAW30099 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Excitation-secretory uncoupling peptide(s) for inhibiting neuro:transmitter release - used particularly for treating
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                                                                                                                                             06-APR-1998 (first entry)
                                                                                                                                                                                                                                          AAW30099
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or less frequent treatments
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                                                                                                                                                                                                                                                                                                                                  peptide;
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Pred. No.
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1.3e-07;
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Neurotransmitter secretion inhibitor #3.

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurotransmitter from neuronal cells and is an excitation secretory uncoupling peptide (I) of at least 20 amino acids (aa) all of which correspond substantially to any one of AAW30097-W30102, or more generally any (I) that inhibits 50% of catecholamine secretion from bovine chromaffin cells at a concentration of 10 microM, especially 0.25 microM, or less. (I) are used, as a replacement for Clostridium toxin, to inhibit release of neurotransmitters from synaptic vesicles, specifically for reducing muscle spasticity. Also (I) may be labelled to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering the drug to neural cells provide targeted drug delivery, e.g. of substance P to brain tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not toxic or induction of apoptosis. Unlike the neurotoxins, (I) are not toxic or induction of apoptosis. Their therapeutic effect lasts for several days or weeks, so lower doses or less frequent treatments are required.
             Homo
                                            synaptosomal
                                                      Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bowlne chromaffin cell; Clostridium toxin; muscle spasticity reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence corresponds to residues 181-206 of the human 25 synaptosomal associated protein (SNAP-25), and is a inhibitor the invention inhibit secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Excitation-secretory uncoupling peptide(s) for inhibiting neuro:transmitter release - used particularly for treating spasticity, and for delivering drugs specifically to neuron spasticity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25.
                                                                                                                      Neurotransmitter secretion inhibitor #1
                                                                                                                                                       06-APR-1998
                                                                                                                                                                                                                  AAW30097 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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             sapiens
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                                                                                                                                                                                                                                                                                                                                                             Conservative
                                          associated
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                                                                                                                                                                                                                  peptide;
                                                                                                                                                     entry)
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                                         protein;
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                                                                                                                                                                                                                                                                                                                                                            Score 83; DE Pred. No. 1.8); Mismatches
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                                          SNAP-25
                                                                                                                                                                                                                                                                                                                                                                         DB 18;
1.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                        Length 26;
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to neural cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurotransmitter from neuronal cells and is an excitation secretory uncoupling peptide (I) of at least 20 amino acids (aa) all of which correspond substantially to any one of AAM30097-W30102, or more generally any (I) that inhibits 50% of catecholamine secretion from bovine chromaffin cells at a concentration of 10 microM, especially 0.25 microM, or less. (I) are used, as a replacement for Clostridium toxin, to inhibit release of neurotransmitters from synaptic vesicles, specifically for reducing muscle spasticity. Also (I) may be labelled to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering the drug to neural cells provide targeted drug delivery, e.g. of substance P to brain tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not toxic or immunogenic and are more readily available. Their therapeutic effect lasts for several days or weeks, so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence corresponds to residues 170\text{-}206 of the human 25 k synaptosomal associated protein (SNAP-25), and is a inhibitory the invention. The agents of the invention inhibit secretion of
            03-JUN-1994;
                                                                                                                                              substrate;
                                                                                                                                                         VAMP; vesicle-associated membrane protein; SNAP-25;
neurotransmitter; neurotoxin; botulinum; botulism; c
                                                                                                                                                                                                  SNAP-25 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Excitation-secretory uncoupling peptide(s) for inhibiting neuro:transmitter release - used particularly for treatin spasticity, and for delivering drugs specifically to neur
                                     02-JUN-1995;
                                                                14 - DEC - 1995
                                                                                       WO9533850-A1
                                                                                                                   Synthetic
                                                                                                                                                                                                                           15-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
                                                                                                                                              antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or less frequent treatments
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                           (first entry)
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           94GB-0011138
                                     95WO-GB01279
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                                                                                                                                                                                                                                                                                Peptide;
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                                                                                                                                               detection;
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Pred.
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2.7e-07;
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to neural cells
                                                                                                                                                          cleavage;
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RESULT 9
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Matches 17
The invention relates to new peptides comprising acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated protein 25). The peptide
                                   Claim 16; Page
                                                                             WPI;
                                                                                                                                                                                                                                             Dermatological; neuroprotective; SNAP-25; synaptosomal-associated neurodegenerative disorder.
                                                                                                                                                                                                                                                                               Human SNAP-25 N-terminal peptide
                                                                                                                                                                                                                                                                                                                   AAB15584;
                                                                                                                                                                                                                                                                                                                                  AAB15584 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The botulinum neurotoxins possess highly specific zinc-endopeptidase activities within their light sub-units. Depending on the neurotoxin type these act to cleave small proteins within the nerve cell which are involved in neurotransmitter release. Antibodies are used in assays which detect cleaved but not uncleaved substrate. Assays for botulinum types A and E use the present sequence as a substrate. The sequence is SNAP-25 protein, residues 137-206.
                                                                                                                                                                                           02-NOV-2000
                                                                                                                                                                                                            WO200064932-A1
                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                 02-MAR-2001
                                                              New
                                                                                               Perez
                                                                                                       Fernandez Ballester GJ, Pla
Viniegra Bover S, Gutierrez
                                                                                                                        Blanes Mira MC,
                                                                                                                                                          23-APR-1999;
                                                                                                                                                                          18-FEB-2000; 2000WO-ES00058
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                     treatment
                                                                                                                                        (LIPO-) LIPOTEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the cleaved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                substrate which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assay for botulinum or tetanus toxin - by combining test cpd. with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES. (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                   peptides containing amino acid atment of neurological disorders
                                                                                                                                                                                                                            sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1996-040249/04
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                                                                                                      Llobregat Hernandez MM,
ter GJ, Planell Cases RU
t, Gutierrez Perez LM, (
                                                                                                                                                                                                                                                                                                                                  peptide;
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Pred. No.
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protein SNAP-25
25). The peptides AAB15581-B15586
                                                                                                                                                                                                                                                     relaxant; neuronal exocytosis modulator; protein 25; facial wrinkle; asymmetry;
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Carbonell
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                                                                                                                       Gil Tebar AI;
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  RESULT 10
AAO15165
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Best Local S
Matches 17
                                                                                                                                                WPI;
                                                                                                       Claim
                                                                                                                                                                                                                   25-SEP-2001;
                                                                                                                                                                                                                                     28-MAR-2002
                                                                                                                                                                                                                                                                                      Cleavage-site
                                                                                                                                                                                                                                                                                                                 Cleavage-site
                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                              Clostridial
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                                                                                                                                                                                 (USME-) US
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The invention comprises clostridial neurotoxin substrate peptides which can serve as fluorescence resonant energy transfer assay (FRET) or quenched-signal substrates in assays for the proteolytic activities of clostridial neurotoxins. The invention further comprises clostridium botulinum neurotoxin substrate peptides that can serve as immobilised substrates (i.e. bound to a solld phase) in assays for the proteolytic activities of clostridial neurotoxins. The clostridial (including the Clostridium botulinum) neurotoxin substrate peptides are useful for detecting the presence of clostridial neurotoxins in a sample (e.g. food or an environmental sample). The present amino acid sequence represents clostridial neurotoxin substrate peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridial neurotoxin substrate; botulinum neurotoxin substr fluorescence resonant energy transfer assay; quenched-signal; clostridial neurotoxin detection; food.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent examples of the peptides of the invention. The peptides have neuronal exocytosis inhibitory activity and are used for treatment of facial wrinkles and asymmetry and pathological neuronal exocytosis mediated pathological disorders and alterations manifested e.g. by spasms and neurological and neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                         clostridial neurotoxin,
                                                                                                                                                                                                                                                                                                                                                             Substrate useful in e.g. an assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200225284-A2
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                                                                                                                                                                                                                                                                                          Page 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDICAL RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AA;
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89..90
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residues by
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                                                                                                                                                                                                                                                                                          48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFECTIOUS DISEASES
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type A Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide is cleaved between these two
type E Clostridium botulinum neurotoxin"
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Pred. No.
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6.9e-07;
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                                                                                                                                                                                              neurotransmitters from synaptic vesibles, specifically for reducing muscle spasticity. Also (I) may be labelled to allow in vivo imaging intracellular distribution of (I). Compounds for delivering the drug neural cells provide targeted drug delivery, e.g. of substance P to brain tumours for induction of apoptosis. Unlike the neurotoxins, (I) not toxic or immunogenic and are more readily available. Their therapeutic effect lasts for several days or weeks, so lower doses or
                                                                                                                                                                                                                                                                                                                                                                                               and is an excitation-secretory uncoupling peptide (I) of at least 20 amino acids (aa) all of which correspond substantially to any one of AAW30097-W30102, or more generally any (I) that inhibits 50% of catecholamine secretion from bovine chromaffin cells at a concentration of 10 microw, especially 0.25 microw, or less. (I) are used, as a replacement for Clostridium toxin, to inhibit release of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the human 25 kD synaptosomal associated protein (SNAP-25), which is an inhibitory agent of the invention. The agents of the invention inhibit secretion of neurotransmitter from neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Excitation-secretory uncoupling peptide(s) for inhibiting neuro:transmitter release - used particularly for treating muscle spasticity, and for delivering drugs specifically to neural cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       excitation-secretory uncoupling peptide; catecholamine secretion; bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25.
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 27-28; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-479986/44.
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                                                                                                                                                                         therapeutic effect lasts less frequent treatments
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  1 Similarity
17; Conserv
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     Conservative
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Score 83; DB 18;
Pred. No. 1.8e-06;
; Mismatches 0;
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Pred. No.
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                                                     Length 206;
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RESULT 12
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                                                                                                                                                                                                                                                                                                        This represents a mouse SNAP-25 polypeptide, a component of the protein polypeptides thought to underlie vesicle docking and fusion. The invention provides rat and human Hrs-2 polypeptides which are ATP-preferring nucleotidase that associate with SNAP-25. For identifying a compound capable of modulating calcium-regulated secretion of secretory vesicles, a SNAP-25 polypeptide can be contacted with a Hrs-2 polypeptide, in the presence and absence of a test compound. The effect of the test compound on the extent of binding between the SNAP-25 and Hrs-2 polypeptides are measured and a compound is identified as effective if its measured effect on the extent of binding is above a threshold level. The products can be used for identifying drugs capable of a fection and a contactor wrongers with a polypeptide of the contactor of the contactor of the capable of the secretory processes.
                                                                                                      of the brain, including affective disorders (e.g. depression), disorders of thought (e.g. schizophrenia) and degenerative disorders ( Parkinson's disease), as well as applications such as anaesthesia. The drugs can also be used therapeutically in other systems such as the endocrine system for treatment of hormonal imbalances, the immune system for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hrs-2 polypeptide; ATP-preferring nucleotidase; SNAP-25; vesicle docking; calcium-regulated secretion; secretory vesicle; secretory process; brain; neurotransmitter release; presynaptic membrane; CNS disorder; depression; parkinson's disease; endocrine system; hormonal imbalance; cell division; thought disorder; schizophrenia; degenerative disorder; anaesthesia; rat;
                                                                                                                                                                                                                    affecting secretory processes, such as neurotransmitter release at the active zones of presynaptic membranes. Such drugs can be used for treating disorders or conditions of the central nervous system by selectively enhancing or inhibiting vesicular release in specific areas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Pages 42-44; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system; antigen processing; immunomodulator; viral processing; central nervous system; vesicular release; affective disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW79198 standard; Protein; 206
                                                               system for treatment of hormonal imbalances, the immune system for intervention in antigen processing, secreted immunomodulators, and viral processing, as well as anti-tumour applications, such as regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secretory vesicles, such as in neurotransmitter release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Hrs-2 nucleotidase - used in assays to identify compounds capable of modulating calcium-regulatory secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV57558.
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                                       trafficking during rapid
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RESULT 14
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                                                                                                                                                                                                  protein of 25 kD (SNAP-25). The invention relates to a method for identifying a compound capable of affecting the binding of a syntaxin binding protein (SBP), e.g. SNAP-25 alpha-SNAP, n-sec1 or VAMP, to syntaxin. The method comprises measuring the effect of the test compound on the extent of binding between the SBP and the SBP-binding site on syntaxin. The method can be used for identifying drugs capable of inhibiting or stimulating neurotransmitter release at the active zones of presynaptic membranes, which may be useful for treating CNS disorders, affective or psychotic disorders, neurodegenerative diseases, hormonal or immunological disorders or tumours.
                                                                                                                                                                                                                                                                                                                         This amino acid sequence represents the mouse synaptosomal-associated protein of 25 kD (SNAP-25). The invention relates to a method for
                                                                                                                                                                                                                                                                                                                                                                                      Screening assay for modulators of syntaxin binding - using peptide comprising binding site of syntaxin, for identifying drugs useful for treating CNS disorders, neuro-degenerative diseases, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS; neurotransmitter; presynaptic membrane; central nervous system; tumour
             AAU00246 standard; Protein; 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse synaptosomal-associated
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                                                                                                                               l Similarity
17; Conserv
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                                                                                                     SNKTRIDEANQRATKML 17
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disease; hor
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Pred. No. 1.8e-06;
                                                                                                                                           Pred.
                                                                                                                                                      Score 83;
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              A
                                                                                                                             Mismatches
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                                                                                                                            DB 19;
1.8e-06;
hes 0;
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                                                                                                                                                      Length 206;
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CC attachment protein receptor) to a cell of the patient, where the SNARE is cresistant to protein receptor) to a cell of the patient, where the SNARE is creabable of inhibiting the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-resistant SNARE) and/or is ceapable of inhibiting the toxin (toxin-resistant SNARE). The protein can be used in a method of treating a patient in need of inhibition of SNARE. CC dependent exocytosis from a cell capable of performing SNARE-dependent ce exocytosis, comprises supplying a fragment, variant, fusion or derivative co of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin cresistant or toxin inhibitory SNARE to the cell of the patient. The toxin cresistant or toxin inhibitory SNARE or a recombinant polynucleotide control of a patient suffering from poisoning or at risk of poisoning control of the suffering from botalism or tetanus. The fragment, control of crecombinant polynucleotide encoding either of these SNARE polypeptides care useful in the manufacture of medicament for the treatment of a cell capable of performing SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. The method of treatment control of a state of the symptoms when most severe and capable of the nation of the sations of the symptoms when most severe and control of the symptoms when most severe and capable of the nation of the sations of the symptoms when most severe and capable of the nations of the symptoms when most severe and capable of the nations of the symptoms when most severe and capable of the nations of the symptoms when most severe and capable of the symptoms w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated protein, SNAP25. The sequence was used to create SNAP-25 double/single point mutants and C-terminal demonstrates used in a new method of treating a patient suffering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating a patient suffering from poisoning or at risk of poisoning a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage-site
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Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents the amino acid sequence of synaptosomal-
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Query Match Best Local Matches

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100.0%; ilarity 100.0%; Conservative (

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Score 83; Pred. No. Mismatches

. 1.8e-06; ches 0;

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Gaps

0

DB 22;

Length 206; Indels

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187 SNKTRIDEANQRATKML 203

SNKTRIDEANQRATKML

17

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0;

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RESULT 15
AAU00252
The sequence represents the amino acid sequence of SNARE homologue, CC synaptosomal-associated membrane protein, hSNAP25a, used during analysis of SNAP-25 SNAP-25 mutants were used in a new method of treating a CC patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, CC where the SNARE is resistant to proteolysis by the toxin (toxin-resistant CC SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory CC SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory CC SNARE). The protein can be used in a method of treating a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis, comprises supplying a fragment, CC variant, fusion or derivative of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is useful in the poisoning or at risk of poisoning by clostridial toxin, e.g. from CC manufacture of an inhibitory SNARE, or a recombinant polynucleotide encoding CC either of these SNARE polypeptides are useful in the manufacture of medicament for the treatment of a patient in need of inhibition of SNARE. CC elevations the streatment of a patient in need of inhibition of SNARE. CC alleviating the symptoms when most severe and taking the patient out of critical state.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE; toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosi synaptosomal-associated protein; hSNAP25a; human; N-ethylmaleimide-sensitive fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU00252 standard; Protein; 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 8; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS00369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolly JO, O'Sullivan GA,
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Query Match

100.0%;

Score

83; DΒ 22;

Length 206;

Sequence

206

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                                    Best Local Similarity Matches 17; Conserv
187 SNKTRIDEANQRATKML
           1 SNKTRIDEANQRATKML 17
                                      Conservative
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Search completed: September 16, Job time: 12.1429 secs

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Perfect score:
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Gapop 10.0 , Gapext 0.5
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    DΒ
SN25_HUMAN
SN2A_CARAU
SN2B_CARAU
SN25_DROME
SN23_HUMAN
SN25_CAEEL
SN33_HOMAN
SN30_ARATH
SC9_FAATH
SC9_FAATT
SC9_FUMAN
SN25_RABIT
SN29_HUMAN
SN25_RABIT
MYH7_RAT
YMP7_YEAST
YMP7_YEAST
YMP7_PIG
MYH6_MOUSE
MYH6_MOUSE
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MYH1_HUMAN
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213540 mesocricetu
212883 homo sapien
202563 rattus norv
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3 sus scrofa
6 mus musculu
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8 arabidopsis
1 caenorhabdi
9 arabidopsis
6 arabidopsis
7 saccharomyc
1 homo sapien
0 oryctolagus
4 rattus norv
6 rattus norv
2 homo sapien
2 homo sapien
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2 oryctolagus
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	O08638 mus musculu	P05661 drosophila	P41114 podocoryne	P40457 saccharomyc		Q9ptd7 xenopus lae					

ALIGNMENTS

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Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,	., Cobley V.E., Collier R.E., Connor R.E., Corby N.	nan J.C., Clamp M., Clark G., Clark L.N., Clark S.	. D . F . ,	riow K.F., Bates K.N., Beard L.M., Beare D.M.,	Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.	P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.	MEDLINE=21638749; PubMed=11780052;	Human;	SEQUENCE FROM N.A.		J. 317:945-954(1996).	2. *:	(synaptosomal-associated protein 25) A and B isoforms in addition to	ticanes contain the core complex protein suad-	Verkuylen A., Cosgr	wish D.R., Macaulay S.L.	94; PubMed=8760387;	PECIES=Human; TISSUE=Skeletal muscle;	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.	L	"Cioning and sequence analysis of the numan SNAP25 cDNA.";	Hashida H., Takanashi N., Sakaki Y.;	94333829; PubMed=8056350;	SSUE=Brain;	SEQUENCE FROM N.A.		Gene 139:291-292(1994).	al protein SNAP-25.";	an cl		MEDITURE 94 156217. PUMPAGE 81 12622.	SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).		D=9606, 9544, 10090, 10116, 9031;	Catarrhini: Hominidae:	Chordata: Craniata:	norveg	sculus (Mouse),	oa mulatta (Rhes	ໝ	7.0	S-SEP-2003 (Rel. 42, Last annotation update)	1991 (Rel. 17, Last	1990 (Rel. 13,	N25_HUMAN	LT 1 _HUMAN

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RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., RA Tracey A., Tromans A.C., Vaudin M., Wall M., Walliams S.A., Wilhiams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RX MEDLINE=2388257; Numbed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wackernan K.J., Malek J.A., Gunaratne P.H.,

RA Rachards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Alteschey R.W., Touchman J.W., Green E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Touchman and mouse cDNA, sequences ";
                                                                                                                                                                                         SEQUENTES PROTECTION OF THE SAME
   SPECIES—Chicken; TISSUE—NULL SPECIES—Chicken; TISSUE—NULL SPECIES—Chicken; TISSUE—NULL SPECIES SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bloom F.E., Wilson M.C.;
"The identification of a novel synaptosomal-associated SNAP-25, differentially expressed by neuronal subpopula J. Cell Biol. 109:3039-3052(1989).
Catsicas S., Wilson M.C.;
                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=Rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oyler
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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F.E., Wilson M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences. Natl. Acad. Sci. U.S.A. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NA sequence and com
414:865-871(2001).
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                                                                                                                                                                          (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J., Smith L. (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                (MAY-1997)
                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6;
                                                                                                                                                                      SNAP-25
2000) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORMS
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                                                                                                                                                                      EMBL/GenBank/DDBJ
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                                                                                                                                                                                                        from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.A.,
                           Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Battenberg
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                           Sanna
                                                                                                                                                                                                                                                                                                                                                                                                                                         SNAP-25B).
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                                                                                                                                                                                                                                                                                                                                                    databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ssociated protein, subpopulations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      databases
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                     P.P.,
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E
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                           Milner
                           R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.";
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Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;
"The 25 kDa synaptosomal-associated protein SNAP-25 is the major
methionine-rich polypeptide in rapid axonal transport and a major
substrate for palmitoylation in adult CNS.";
J. Neurosci. 12:4634-4641(1992).
                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression of a concides wit terminals coincides wit terminals coincides with Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brain Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jacobsson G., Piehl F., Bark I.C., Zhang X., Meister B "Differential subcellular localization of SNAP-25a and transcripts in spinal motoneurons and plasticity in exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96346613; PubMed=8738135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=Rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PALMITOYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bark I.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93389738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: NEURONS OF THE NEOCORT!
PIRIFORM CORTEX, ANTERIOR THALAMIC NUCLEI,
GRANULE CELLS OF THE CEREBELLUM.
PTM: PALMITONIAMON
          L; L19760; AAC37545.1; -...
L; D21267; BAAA22370.1; -...
L; AL023913; CAB42860.1; -...
L; AL023913; CAC34534.1; -...
L; AF240770; AAF64477.1; -...
L; BC018249; AAH18249.1; -...
L; M57957; AAA49072.1; -...
L; AF245227; AAF81202.1; -...
L; AB003991; BAA20151.1; -...
L; AB003992; BAA20152.1; -...
L; AB003992; BAA20152.1; -...
L; AB003992; BAA2015.1; -...
                                                                                                                                                                                                                                                                                                                                                                                            PTM: PALMITOYLATED.
SIMILARITY: BELONGS T
SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event-Alternative splicing; Named isoforms=2; Comment=Isoforms differ by the usage of two homologous exons (5a and 5b) which encode fo and differ only in 9 positions out of 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins involved in vesicle docking SUBUNIT: Binds to syntaxin-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              runction: tsnare neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=SNAP-25a;
IsoId=P13795-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=SNAP-25b;
IsoId=P13795-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                injury.
                                                                                                                                                                                                                           L19761;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol.
                                                                                                                                                                                                                                                                                                                                                                                     TY: BELONGS TO THE SNAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : tSNARE involved in the molecular regulation of nsmitter release. May play an important role in the function of specific neuronal systems. Associates
                                                                                                                                                                                                                         AAC37546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brain Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed-8377193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synaptogenesis.";
.S.A. 88:785-789(1991).
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                                                                                                                                                                                                                                                                                                                                                                                           SNAP-25 FAMILY.
NARE coiled-coil homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
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protein.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEOCORTEX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                             as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o alternative for positions
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                                                                                                                                                                                                                                                                                                                                                   collaboration
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RESULT 2
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Actinopterygii; Neopterygii; Teleostei;
Cyprinidae; Carassius.
NCBI_TaxID-7957;
[1]
                                                                                                                                                                       Interpro; IPR000928; SNAP-25.
Interpro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
                                                                                                                                                                                                                                                  EMBL; L22973; AAA16537.1; PIR; I50480; I50480.
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01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Synaptosomal-associated protein 25A (SNAP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SN2A_CARAU
P36977;
                                                                                                                                                                                                                                                                                                                          or send
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       SEQUENCE
                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Multiple loci for synapse protein SNAP-25 in the tetraploid
                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED VESICLE DOCKING AND MEMBRANE FUSION.
SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION
SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE NERVE
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                                                                                                                           SM00397; t_SNARE;
E; PS50192; T_SNAR
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an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A
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                                                                                                    Neurone; Repeat;
                                 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TERMINAL.
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                                                                                                                         T_SNARE; 2.
                                                   81
200
       22843
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       Œ.
                              T-SNARE C
T-SNARE C
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 2.7e-62;
; Mismatches 0;
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     458BBECFCFC09189
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                                                COILED-COIL
                                                                        coil; Multigene family
COILED-COIL HOMOLOGY 1
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                                                   HOMOLOGY
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RESULT 3
SN2B_CARAU
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Best Local
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01-JUN-1994
15-SEP-2003
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carassius auratus (Goldfish).
Bukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Carassius.
                         Synaptosome;
DOMAIN
                                                                  InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                             goldfish.";
Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Creat
01-JUN-1994 (Rel. 29, Last
15-SEP-2003 (Rel. 42, Last
Synaptosomal-associated pro
                                                       PROSITE; PS50192;
                                                                                                                        EMBL; L22976; AAA16538.1; -. PIR; I50481; I50481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94068448; PubMed=8248151; Risinger C., Larhammar D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SN2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNAP-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P36978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                PIRIFORM CORTEX, ANTERIOR THALAMIC NUCLEI, PONTINE NUCLEI, FRANULE CELLS OF THE CEREBELLUM.
SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                             THE NERVE TERMINAL.
TISSUE SPECIFICITY: NEURONS OF THE
PIRIFORM CORTEX, ANTERIOR THALAMIC
                                                                                                                                                                                                                                                                                                                                                   C. Natl. Acad. Sci. U.S.A. 90:10598-10602(19
ENCTION: MAY PLAY AN IMPORTANT POLITY IN THE SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH VESICLE DOCKING AND MEMBRANE FUSION. SUBCELLULAR LOCATION: COMPLEXED WITH MACROMORY NEURONAL PROPERTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _CARAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                       iple loci for synapse protein SNAP-25 in the tetraploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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; Neurone;
19 81
137 199
85 92
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                                                                 t_SNARE;
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                                                    T_SNARE; 2.
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199
92
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93.2%;
                                       NARE; 2.
Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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annotation update)
otein 25B (SNAP-25B).
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; Coiled coil; Multigene family. T-SNARE COILED-COIL HOMOLOGY 1. T-SNARE COILED-COIL HOMOLOGY 2. CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Craniata;
Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 974; DB 1; Pred. No. 1.9e-57;
                                                                                                                                                                                                                                                                                                                                                                                        90:10598-10602(1993).
POTE IN THE SYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                         WITH MACROMOLECULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; E
Ostariophysi;
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i; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                        ELEMENTS
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RESULT
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Best Local S
Matches 184
                                      PIR; 150552; 150552.
InterPro; IPR000928; T_SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                  use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         This SWI
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CARBOHYD
                                                                                                                                                                                                                                                                                                                   Risinger C., Blomqvist A.G., Lundell I., Lambertsson A
Massel D., Pieribone V.A., Brodin L., Larhammar D.;
"Evolutionary conservation of synaptosome-associated p
(SNAP-25) shown by Drosophila and Torpedo cDNA clones.
J. Biol. Chem. 268:24408-24414(1993)
-1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPT
SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEIN
VESICLE DOCKING AND MEMBRANE FUSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synaptosomal-associated protein 25 (SNAP-25).
Torpedo marmorata (Marbled electric ray).
Torpedo marmorata (Marbled electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Cl
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; E
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Synaptosomal-associated protein 25 (SNAP-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SN25
                              Synaptosome;
                                                                                                                          EMBL; L22020; AAA49284.1;
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Electric lobe;
MEDLINE=94043281; PubMed=8226991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SN25_TORMA
P36976;
                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Everopean Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE SNAP-25 FAMILY. SIMILARITY: Contains 2 t-SNARE coiled-coil homology
                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: COMPLEXED THE NERVE TERMINAL.
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185
203
 ; Neurone;
23 8
147 20
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209
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185
22664
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                            Repeat;
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N-LINKED (GLCNAC. ..) (POTENTIAL)
; 8DFBBEDBED37D6D7 CRC64;
T-SNARE COILED-COIL
T-SNARE COILED-COIL
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Pred. No. 8.4
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              HOMOLOGY
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Matches 164
                                                         entities re
or send an
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01-JUN-1994
15-SEP-2003
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SEQUENCE
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between
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Gene 194:169-177(1997).
-i- FUNCTION: MAY PLAY AN IMPORTANT ROLE I
SPECIFIC NEURONAL SYSTEMS. ASSOCIATES
VESICLE DOCKING AND MEMBRANE FUSION.
EMBL;
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Neoptera; Endopterygota; Dipter;
Ephydroidea; Drosophilidae; Dro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=97417485; PubMed=9272858;
Risinger C., Deitcher D.L., Lunde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Risinger C., Blomqvist A.G., Lundell I., Lambertsson / Nassel D., Pieribone V.A., Brodin L., Larhamar D.; "Evolutionary conservation of synaptosome-associated (SNAP-25) shown by Drosophila and Torpedo cDNA ciones J. Biol. Chem. 268:24408-24414(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94043281; PubMed=8226991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Complex gene organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                    TISSUE SPECIFICITY: EXCLUSIVELY FOUND IN BRAIN AND GANGLIA. SIMILARITY: BELONGS TO THE SNAP-25 FAMILY. SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                          European
                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: THE NERVE TERMINAL.
                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
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                     L22021;
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                                                         non-profit institutions as long and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKADSNKTRIDEANQRATKML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 29, Created)
(Rel. 29, Last sequence up
(Rel. 42, Last annotation
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                                                                                                                                            Bioinformatics Institute.
  AAA16059.1;
AAB39757.1;
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23652 MW;
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of synaptic |
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Drosophila.
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Pred. No. 1.
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                                                                                (See http://www.isb-sib
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                                                                                                                       There are no restrictions ing as its content is in
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S WITH PROTEINS 1
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                                                                                                 Usage
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Best Local S
Matches 124
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TISSUE-Neutrophils;
MEDLINE-9722437; PubMed-9070898;
MOILINEO F., Lazo P.A.;
MIDITINEO F., Lazo P.A.;
"Identification of two isoforms of
SNAP-23 in human neutrophils and HI
                                                                                                 Ravichandran V., Chawla A., Roche P.A.; "Identification of a novel syntaxin- and synaptobrevin/VAMP-binding protein, SNAP-23, expressed in non-neuronal tissues."; J. Biol. Chem. 271:13300-13303(1996).
                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                        SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                              MEDLINE=96278745;
                                                                                                                                                                               TISSUE=B-cell
                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                     SNAP23
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                                                                                                                                                                                                                          NCBI_TaxID=9606;
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L; U81148; AAB39757.1; JOINED.
L; U81149; AAB39757.1; JOINED.
L; U81150; AAB39757.1; JOINED.
L; U81151; AAB39757.1; JOINED.
L; U81152; AAB39757.1; JOINED.
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148
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212
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                                                                                                                                                                                             N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑĄ;
                                                                                                                                                              PubMed=8663154;
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210 T
99 C
23685 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t; Coiled coil.

T-SMARE COILED-COIL H

T-SMARE COILED-COIL H

CYS-RICH.

BDC90649A1AF3AC8 CF
                                                                                                                                                                                           SNAP-23A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 618.5;
Pred. No. 3.7e
29; Mismatches
                                                                        SNAP-23A
                                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae
 of the
HL-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r secretion; Ne e docking; NAS e fusion; NAS.
                                                                                                                                                                                                                                                                                                               ion update)
(SNAP-23)
                                                                          AND
 vesicle-membrane
cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .7e-34;
                                                                       SNAP-23B)
                                                                                                                                                                                                                                      Hominidae;
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                                                                                                                                                                                                                                                                                                               (Vesicle-membrane
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               protein
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Faha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Generation and initial analysis of more than 15,000 full-length
The Generation and initial analysis of more than 15,000 full-length
THE GENERAL MEMBRANE FUSION MACHINERY AND AN IMPORTANT REGULATOR
CC OF TRANSPORT VESICLE DOCKING AND FUSION.
CC SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS AND
CC SYNAPTOBREVILL BLOOKING AND LOCALITED TO THE BLOOKING AND MEMBRANE
                                                                                                                                                                                                                  EMBL; U55936; AAC50537.1; -... EMBL; Y09567; CAA70760.1; -... EMBL; Y09568; CAA70761.1; -... EMBL; BC00148; CAA09644.1; -... EMBL; BC000148; AAH00148.1; -... EMBL; BC022806; AAH02890.1; -... EMBL; BC02280; AAH22890.1; -... PIR; JC5296; JC5297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem.
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
Nadal M., Area E., Mollinedo F., Estivill X., Lazo P.A.;
"Exon organization and chromosomal localization of human synaptosomal associated protein-23 (SNAP-23) gene and generation of isoforms by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
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GO: GO:0005482; C:plasma membrane; TAS
GO: GO:0005803; C:secretory vesicle; T.
30; GO:0005482; F:vesicle targeting; Ti
O; GO:0006944; P:membrane fusion; TAS
O; GO:0006903; P:non---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Cervix, Placenta, and Testis; MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: MAINLY LOCALIZED ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=SNAP-23b;
IsoId=000161-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=SNAP-23a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=000161-1;
                                                                                                                                                                                                   C5297; JC5297.
HGNC:11131; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A. (ISOFORM
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                     vesicle targeting;
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                                                                    e; TAS.
e; TAS.
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RM MEDLINE-21016719; Pubmed-11130712;

Rheologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Rheologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Rheologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Rheologis A., Ecker J.R., Palm C.J., Cheuk R.F., Chin C.W.,

Rheologis A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Rheologis A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Rheologis A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Rheologis A., Chao Q., Chen H., Cheuk R.F., Fong J. Fujii C.Y.,

Rheologis A., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Rheologis A., Cheo M., Fong J.-D., Fong B., Fujii C.Y.,

Rheologis A., Cheo M.F., Fong J.-D., Fong B., Fujii C.Y.,

Rheologis A., Cheo M.F., Fong J.-D., Fong B., Fujii C.Y.,

Rheologis A., Cheo M.F., Khasen N.F., Hughes B., Huizar L.,

Rham Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Khan A., Liam B.,

Rheologis A., Cheo M., Rooney T., Rowley D.,

Rheologis A., Cheo M., Rooney T., Rowley D.,

Rheologis A., Schwartz J.R., Shinn R., Southwick A.M.,

Rheologis A., Cheo M., Rooney T., Southwick A.M.,

Rheologis A., Cheo M., Rheologis A., Rheologis A.,

Rheologis A., Cheo H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Rheologis A., Cheo H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Rheologis A., Cheo M., Rheologis A.,

Rheologis A., Cheo H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Rheologis A., Cheo M., Rheologis A.,

Rheologis A., Cheo H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Rheologis A., Cheo M., Rheologis A.,

Rheologis A., Cheo H., Rhe
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Best Local S
Matches 124
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28-FEB-2003 (Rel. 42, Last sequence update)
28-FEB-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Putative SNAP25 homologous protein SNAP30 (AtSNAP30) (Synaptosomal-associated protein SNAP25-like 3).
SNAP30 OR ATIGI3890 OR F16A14.10.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
   Utterback
Wu D., Yu
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SEQUENCE
                                                         Sun H.,
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SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0006892; P:post Golgi transport; InterPro; IPR000928; SNAP-25. InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
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                           Tallon L.J., Tambunga G., Toriumi M.J., Town C.D ck T., Van Aken S., Vaysberg M., Vysotskaia V.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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   Vaysberg M.,
Venter J.C.,
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Pred. No. 1.4
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T-SNARE COILED-COIL HOMOLOGY
R -> S (in isoform SNAP-23b).
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A -> V (IN REF. ]
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                                                            C.b.
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Best Local
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28-FEB-2003
28-FEB-2003
15-SEP-2003
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulsc Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M. Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latreille P., Lightning J., Lloyd C., Mortinore B., O'Callaghan Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownke Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AC068197; AAF79396.1; -
PIR; A86272; A86272;
InterPro; IPR000727; T_SNARE.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 1.
                                                                                                                             STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                       Eukaryota; Me
Rhabditidae;
                                                                                                                                                                                                                                                   Hypothetical protein K02D10.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Transport; Protein transport; Membrane; Coiled coil; Multigene family.

DOMAIN 198 260 T-SNARE COILED-COIL HOMOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as low
modified and this statement is not remove
entitles requires a license agreement (So
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                         YMQ5_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: Vesicle trafficking protein that functions
secretory pathway (By similarity).
-i- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
-i- SIMILARITY: Contains 1 t-SNARE coiled-coil homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence and analysis of chromosome 1 of the thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
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62; Conserv
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e; Peloderinae;
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(Rel. 41, Last seq
(Rel. 42, Last ann
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                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                      Nematoda;

    Last sequence update)
    Last annotation update

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Caenorhabditis.
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Pred. No. 3e-10;
9; Mismatches
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D55EE680CEFE02C4 C
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                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-FEB-2003 (Rel. 42, Last annotation update)
15-FEP-2003 (Rel. 42, Last annotation update)
SNAP25 homologous protein SNAP33 (AtSNAP33) (Synaptosomal-associated protein SNAP25-like 1) (SNAP-25 like protein 1) (Snap25a).
SNAP33 OR SNAP33B OR AT5G61210 OR MAF19_210 OR MAF19.2.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.:
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
-!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston
Wohldman P
"2.2 Mb of
                                                                                                                                                                                                                              SN33_AR
Q9S7P9;
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                          STRAIN=cv. Landsberg erecta, and c
MEDLINE-21490313; PubMed-11591731;
               Heese M.,
                                                     SEQUENCE FROM N.A.,
                                                                               NCBI_TaxID=3702
                                                                                                                                                                                                                                                            ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
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InterPro; IPR000727; T_SNARE.
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E; PS50192; T_SNARE; 2.
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179
277
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31115 MW;
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28.0%;
               Sticher L.,
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Pred.
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                Wick
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No. 3.
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STRAIN-cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theol
"RIKEN Arabidopsis full length cDNA clones
"RIKEN Arabidopsis full length CDNA clones
"RIKEN Arabidopsis full length CDNA clones
"CSD consortium (Salk/Stanford/PGEC).";
                                                                                                                                                                                                          Mechanical Stimulation.";

Plant Physiol. 132:343-351(2003).

-I- FUNCTION: T-SNARE involved in diverse vesicle trafficking a membrane fusion processes, including cell plate formation. function in the secretory pathway.

-I- SUBUNIT: Interacts with the cytokinesis-specific syntaxin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim C.J., Chen H., Cheuk R.F., Shinn P., Bowser L., Carninci P., Chan M., Chang C.H., Dale J.M., Deng J.M., Bayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.M., Tang C.C., Toriumi M.J., Wallender E.K., Wong C. Wu H.C., Yamada K., Yu G., Yuan S., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional characterization of the KNOLLE-interacting AtSNAP33 and its role in plant cytokinesis.";
J. Cell Biol. 155:239-249(2001).
                          This
                                                                                                                                                                                                                                                                                                      PubMed=12746539;
Wick P., Gansel
Sticher L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidops
Sequence features of the regions
physically assigned Pl clones.";
                                                                                                                                                          <del>-</del>
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Tabata S.;
             between
                                                                                                                                                                                                                                                                                           "The Expression of the
                                                                                                                                                                                                                                                                                                                                                                     Kargul J., Gansel X., Tyrrell "Protein-binding partners of FEBS Lett. 508:253-258(2001).
                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION,
MEDLINE-21576055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ecker
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                                                                                                                                                                                                                                                                                                                                               INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Arabidopsis ORF clones.";
                                                and localy only by mechanical stresses.
MISCELLANEOUS: Specifically cleaved by
BotN/A and BotN/E.
SIMILARITY: BELONGS TO THE SNAP-25 FAMI
SIMILARITY: Contains 1 t-SNARE coiled-c
                                                                                                                tips, ovules, very young leaves, vascular tissue, stipules and the abscission and dehiscence zones INDUCTION: Localy and systemicaly induced by path
                                                                                                                                                    and with SYP121.
SUBCELLULAR LOCATION: Membrane-associated.
endomembrane compartment and cell plate in
TISSUE SPECIFICITY: Ubiquitous, with a stre
            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM
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ra Y., Sato S.,
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o the EMBL/GenBank/DDBJ
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                                                                                                                                            leaves, vascular tissue,
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Best Local S
Matches 60
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EMBL;
  This
                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
SNAP25 homologous protein SNAP29 (AtSNAP29) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB006696; BAB10383.1; -.
EMBL; AY057627; AAL15258.1; -.
EMBL; AY085322; AAM62553.1; -.
EMBL; AY141994; AAM98258.1; -.
EMBL; AY141994; AAM98258.1; -.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; T_SNARE.
Pfam; PF00835; SNAP-25; T.
PROSITE; PS50192; T_SNARE; 1.
Collagorit, Wollision; Transport; Protein transport; Membrane;
                                                                       -I-
                                                                                                             Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome
features of the 1.6 Mb regions covered by twenty physica
                                                                                                                                                    STRAIN=cv. Columbia;
MEDLINE=97471969; PubMed=9330910;
Sato S., Kotani H., Nakamura Y.,
                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                       protein SNAP25-like 2).
SNAP29 OR ATSG07880 OR MXM12.11 OR F13G24.80.
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DOMAIN 235 297 T-SNARE COILED-COIL HOMOLOGY.

SEQUENCE 300 AA; 33644 MW; 685A0484608C6DE7 CRC64;
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                                                                                                  P1 clones
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                           Q9SD96;
                                                                                                                                                                                                                                                                                                                                                                                          SN29
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                         N Res. 4:215-230(1997).
FUNCTION: Vesicle trafficking protein that functions in the secretory pathway (By similarity).
SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
SIMILARITY: Contains 1 t-SNARE coiled-coil homology domain.
                                                                                                                                                                                                                                                                                                                                                                                        ARATH
  SWISS-PROT
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X92419; CAB52582.1; -.
Y13198; CAC79615.1; -.
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27.3%;
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L.5e-08;
les 71;
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RESULT 11
SEC9_YEAST
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                                                                                                                                                               "Sec9 is a SNAP-25-like component of
be the effector of Sec4 function in e
Cell 79:245-258(1994).
                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Protein transport protein SEC9.
SEC9 OR HSS7 OR YGR009C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institute. There are trestrictions modified and this statement is not removed. Usage hy and the statement is not removed. Usage hy and the statement is not removed.
                                                                                                              Hebling U., Hofmann B., Delius H.; Submitted (MAY-1996) to the EMBL/Ge-i- FUNCTION: COMPONENT OF A SNARE
                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                      This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL
                                                            Brennwald P., Kearns
Bankaitis V., Novick
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-95042722; PubMed=7954793;
                                                                                                                                                                                                                                                                                                                                                                              P40357;
01-FEB-1995
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EMBL; AB005249; BAB09952.1; -.
PIR; T45613; T45613.
InterPro; IPR000727; T_SNARE.
           the
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                        SEC9
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European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                            TO YEAST YMR017W. Contains 2 t-SNARE coiled-coil homology domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transport; Membrane; Coiled coil; Multigene 248 T-SNARE COILED-COIL HOMOLOGY.
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                                                                                                                                                                                                                             Champion
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                                                                                                            EMBL/GenBank/DDBJ databases
A SNARE COMPLEX THAT MAY BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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exocytosis.";
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                                    a collaboration
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                                                                                                                EFFECTOR
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                          outstation
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Best Local S
Matches 56
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000
30-MAY-2000
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 42, Last annotation update)
Synaptosomal-associated protein 29 (SNAP-29) (Vesicle-membrane fusion protein SNAP-29) (Soluble 29 kDa NSF attachment protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SN29
                                                                                      TISSUE=Pancreas;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                              SEQUENCE
                                                                                                                                                                Submitted
                                                                                                                                                                                              SEQUENCE FROM N.A. Schardt A., Kraeme
                                                                                                                                                                                                                                                                                     Scheller R.H.;
                                                                                                                                                                                                                                                                                                 Steegmaier M., Yang
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro: IPR000727; T_SNARE.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L34336; AAA35034.1; -.
EMBL; Z72794; CAA96992.1; -.
PIR; A55100; A55100.
SGD; S0003241; SEC9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entitles requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       MEDLINE=99069409;
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                              FROM
                                                                                                                                                            A., Kraemer E.-M., Werner H., Nave K.-A.; organization of the human SNAP29 gene."; organization to the EMBL/GenBank/DDBJ dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and this statement is not removed requires a license agreement (See
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588
651 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                   PubMed=9852078;
ng B., Yoo J.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   650 T
73623 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Coiled coil.
496 T-SNARE COILED-COIL
650 T-SNARE COILED-COIL
73623 MW; EA314D73D20A10C7 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.7%;
25.1%;
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                     Huang
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                                                                                                                                                                                                                                                                                                     Shen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 88
                                                                                                                                                                                                                                                                   family.";
                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
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                                                                                                                                                                                                                                                                                                     Yu
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                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                         153
                                                                                                                                                              95
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                                                                                                                                                                                                                                                                   S
                                                       VSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKM
                       LSMGLGRLKDIALGMQTEIEEQDDILDRLTTKVDKLDVNIKSTERKVRQL
                                                                                          AISTSKEQEAKYQASHPNLRKLDDTDPVPRGAGSAMSTDAYPKNPHLRAYHQKIDSNLDE
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergreen E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Wazny D.M., Sodergreen E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman M.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,
T. Generation and initial analysis of more than 15,000 full-length
Thuman and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF115436; AAD11436.1; -. EMBL; AF278704; AAF91421.1; -. EMBL; BC009715; AAH09715.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IS CYTOPLASMIC.

'ITISSUE SPECIFICITY: FOUND IN BRAIN, HEART, KIDNEY, LIVER, LIPER, LIVER, LIVER, LIVER, LIVER, LIVER, SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.

-!- SIMILARITY: Contains 1 t-SNARE coiled-coil homology domain.
                                                                                                                                                                                                                                                                                                                                                                                                     Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro: IPR000928; SNAP-25.
Interpro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: INVOLVED IN MULTIPLE MEMBRANE TRAFFICKING STEPS
-i- SUBURIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS.
-i- SUBCELLULAR LOCATION: APPEARS TO BE MOSTLY MEMBRANE-BOUND PROBABLY VIA INTERACTION WITH SYNTAXINS, BUT A SIGNIFICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005886; C:plasma membrane; TAS.
GO:0005484; F:SNAP receptor activity;
GO:0006887; P:exocytosis; TAS.
GO:0006944; P:membrane fusion; TAS.
GO:0006903; P:non-selective vesicle ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W; HGNC:11133;
604202; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                PF00835; SNAP-25; 1.
'; SM00397; t_SNARE; 2.
TE; PS50192; T_SNARE; 1.
                                                                                                                                                                                                                    60;
                                                                                                                                                                                                                                             Similarity
                                                    MDQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARVVDE
                                                                                                                                       ADMRNEL-EEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEG
  VDKMDQDLKISQKHINSIKSVFGGLV---NYFKSKPVETPP---EQNGTLTSQPNNRLKE
                                                                                                        ADRQQYLRQEVLRRAEATA----ASTSRSLALMYESEKVGVASSEELARQRGVLERTEKM
                                                                                                                                                                                                                                                                                                                       196
258 AA;
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                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                           Synaptosome; Coiled coil; Membrane.
107 COILED COIL (POTENTIAL).
258 T-SNARE COILED-COIL HOMOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNAP29
                                                                                                                                                                                                                                                                                                                       258 T
28970 MW;
                                                                                                                                                                                                                                          15.8%;
26.1%;
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                                                                                                                                                                                                         Pred. No. U.UU
3; Mismatches
                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                          7E1CDBA22D6F5A3C CRC64;
                                                                                                                                                                                                                                                                166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               targeting;
                                                                                                                                                                                                                                                                      DВ
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                                                                                                                                                                                                                                             0002
                                                                                                                                                                                                                    85;
                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                    Indels
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Mullahy S.J
Maratne P.H.,
Maratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scheetz
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Т.,
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01-NOV-1997
01-NOV-1997
16-OCT-2001
MEDLINE=90016823; PubMed=2798112;
Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.
"Complete nucleotide sequence of full length cDNA
cardiac myosin heavy chain.";
                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                   MYH7_RAT
P02564;
                                                                SEQUENCE FROM N.A.
                                                                                                                                                   Myosin heavy
                                                                                                                                                                           21-JUL-1986
01-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loewy A., Liu W.-S., Baltinger C., Willard M.B.; "The major 35S-methionine-labeled rapidly transported (superprotein) is identical to SNAP-25, a protein of s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; verceuraca, problemanialia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synaptosomal-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, AND CHARACTERIZATION.
STATE THE TEST CHARACTERIZATION.
                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                  16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000928; SNAP-25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (superprotein) is identical terminals.";
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                                                    ISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INCUISCI: 11:3412-3421(1991).

Neurosci: 11:3412-3421(1991).

- FUNCTION: INVOLVED IN THE MOLECULAR REGULATION OF NEUROTRANSMITTER RELEASE. MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN VESICLE DOCKING AND MEMBRANE FUSION (BY SIMILARITY).

VESICLE DOCKING AND MEMBRANE FUSION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE NERVE TERMINAL.

PTM: THE N-TERMINUS IS BLOCKED SIMILARITY: BELONGS TO THE SNA
                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00835; SNAP-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR SNAP.
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                    MLQLVEE-SKDAGIRTLVMLDEQGEQLERIEEGMDQINKDMKEAEKNLTDLGKFCGLCVC
                                                                                                                                                                                                                                                                                                 PCNKLKSSDAYKKAWGNNQDGVVASQPARVVDEREQMAISGGFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synaptosome
                                                                                                                                                                                                                                                                                                                          MLQLVEESSKDAGIRXLVMLDEQGEQLE----
                                                                                                                                                      (Rel. 01, Created)
(Rel. 12, Last sequence update)
(Rel. 40, Last annotation update)
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(Rel.
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                    chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                     45
                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                              STANDARD;
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40,
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                                                                                                                                                                                                                                                                                                                                                                                                                       6064 MW;
                                                                                                                                                 cardiac muscle beta isoform (MyHC-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                     30
46
50
                                                                                                    Rodentia;
                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                   14.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                         Taylor D., Leinwand L.A.;
                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                 Score 156.5; DB 1
Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                       00014F740FEB29C5 CRC64;
                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNAP-25
                                                                                                                                                                                                                                                                          ----RVVDEREQMAISGGFIR 45
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SNAP-25) (Super protein) (SUP)
                                                                                                                                                                                                                1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
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                                                                                                                                                                                                                AA
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                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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                for
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                                                                                                    Murinae; Rattus
               rat beta
                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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EMBL; X15939; CAA34065.1;
EMBL; J00752; AAA41554.1;
EMBL; M32698; AAA41659.1;
PIR; S06006; S06006
HSSP; P08799; IMND.
                                                                                                         Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement entitles requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFRAGMENT (S2).

-i- MISCELLANGOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST'
-i- MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
-i- SIMILARITY: Contains 1 myosin-like globular head dom:
-i- SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUR. HEART J. 5:181-191(1984).

EIR. HEART J. 5:181-191(1984).

II. FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

SUBCELLULAR LOCATION: TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CHARACTERISTIC FOR ALPHA HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McNailly E.M., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.; "Full-length rat alpha and beta cardiac myosin heavy chain sequences. Comparisons suggest a molecular basis for functional differences."; J. Mol. Biol. 210:665-671(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic
[2]
                             Myosin; Muscle protein; Coiled coil; Thick filament;
ATP-binding; Methylation; Alkylation; Multigene famil
                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (or send an email to license@isb-sib.ch)
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"Molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          availability."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and under pathological conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in the adult heart.";
Nature 297:659-664(1982).
                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                              InterPro; IPR004009; InterPro; IPR002928;
                                                                                                                                                                                                                                               InterPro; IPR001609;
                                                                                                                                                                                                                                                                InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cardiac myosin heavy chain isozymic transitions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-85179510; PubMed-6241892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1871-1935 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90133919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISCUSSION OF SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN AFFASE ACTIVITY. MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER SPLIT EURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SI
                                                             ; SM00015; IQ; 1.
; SM00242; MYSC; 1
TE; PS50096; IQ; 1
                                                                                                                                                                              PF00612; IQ; 2.
PF00063; myosin_head; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=2614840;
                                                                                                                                                                                                              Myosin_tail.
                                                                                                                                                                                                                                                myosin_head.
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MYOSIN HEAD-LIKE
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entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                "GS32, a novel Golgi SNARE of 32 kDa, interacts syntaxin 6.";
MOL. Biol. Cell 10.11.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99096689; Pubmed-9880331;
Wong S.H., Xu Y., Zhang T., Griffiths G.,
Seow K.T., Hong W.;
Seow K.T., Hong W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Synaptosomal-associated protein 29 (SNAP-29) (Vesicle-membrane fusion protein SNAP-29) (Soluble 29 kDa NSF attachment protein) (GS32).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Z2P6;
30-MAY-2000
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TISSUE SPECIFICITY: Widely expressed.
TISSUE SPECIFICITY: Widely expressed.
SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
SIMILARITY: Contains 1 t-SNARE coiled-coil homology domain.
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                                                                                                                                                                                                                               Biol. Cell 10:119-134(1999).
SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS.
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ALKYLATION (SH-1) (POTEN
ALKYLATION (SH-2) (POTEN
IRK -> VRR (IN REF. 3).
D -> H (IN REF. 3).
N -> K (IN REF. 3).
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ACTIN-BINDING.
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(POTENTIAL).
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Matches 48
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SMART; SM00397; t_SNARE; 2.

PROSITE; PS50192; T_SNARE; 1.

Protein transport; Synaptosome; Coiled coil.

DOMAIN 195 257

T-SNARE COILED-COIL HOMOLOGY.

SEQUENCE 257 AA; 29070 MW; 9B9BC1A351CB1A3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000928; SNAP-25
InterPro; IPR000727; T_SNARE
                               177
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232 ILDRLTTKVDKLDVNIKSTEKKVRQL
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48; Conserv
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Pred. No. 0.0085;
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257
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Search completed: September 16, Job time: 30.4286 secs 2003, 19:27:06

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Q9y6x9 homo sapien	P45125 haemophilus			P43007 homo sapien				P17247 xenopus lae		P77367 escherichia	Q09841 schizosacch

ALIGNMENTS

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SNUB_CARAU

SNUB_CA
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InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
SMART; SM00397; t_SNARE; 2.
PROSITE; PS50192; T_SNARE; 2.
  SN25_HUMAN
P13795; P36974;
                                                                                                                                                                                   Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.

DOMAIN

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7-SNARE COILED-COIL HOMOLOGY 2.

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CYS-RICH.
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Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                   send an email to license@isb-sib.ch).
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SIMILARITY: Contains 2 t-Snare coiled-coil homology domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
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                                                                         192 EANQRATK 199
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RA Deloukas P., Matthews L. H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
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RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Hammond S., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hunt S.E., Ming A., Knights A., Laird G.K., Lawlor S.,
RA Hammond S., Harley J.L., McConnachie L.J., McLay K., Wchurray A.A.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Phillimore B.J.C.T., Prathalingum S.R., Plumb R.W., Ramay H.,
RA Swann R.M., Sycamore N., Taylor R., Teer L., Thomas D.W., Thorpe A.,
RA Kay M.P., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilneing L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Romers T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., & Frenkel M.J., Ward C.W., "Insulin-responsive tissues contain the core complex (synaptosomal-associated protein 25) A and B isoforms syntaxin 4 and synaptovevins 1 and 2."; Biochem. J. 317:945-954(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao N., Hashida H., Takahashi "Cloning and sequence analysis Gene 145:313-314(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bark I., Wilson M.C.;
"Human cDNA clones encoding terminal protein SNAP-25.";
Gene 139:291-292(1994).
[2]
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01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96332494; PubMed=8760387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat)
Gallus gallus (Chicken)
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10116, 9031;
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                                                                           analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
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man SNAP25 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNAP-25B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complex protein SNAP-25 isoforms in addition to
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                                                                         human
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Alafaci
                                                                           chromosome
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SEQUENCE FROM

.mulatta; N.A.

TISSUE-Hippocampus,

м.ј.,

Smith

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
In Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
      MEDLINE-31100552; PubMed-1281490;
MEDLINE-31100552; PubMed-1281490;
Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;
"The 25 kDa synaptosomal-associated protein SNAP-25 is the major methionine-rich polypeptide in rapid axonal transport and a major substrate for palmitoylation in adult CNS.";
J. Neurosci. 12:4634-4641(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Mouse; STRAIN-C57BL/6; T
MEDLINE-22388257; PubMed-1247793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The identification of a novel synaptosomal-associated protein, SNAP-25, differentially expressed by neuronal subpopulations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=MOUSE: STRAIN-BALB/C;
MEDLINE=90078337; PubMed=2592413;
Oyler G.A., Higgins G.A., Hart R.A.,
Bloom F.E., Wilson M.C.;
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SPECIES-Chicken; TISSUE-Retina;
MEDLINE-91126080; PubMed-1992470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=Rat; TISSUE=Brain;
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                                                                                                            SPECIES-Rat;
                                                                                                                           PALMITOYLATION.
                                                                                                                                                                      "Structure of the chicken gene for encoding distinct isoforms of the p
                                                                                                                                                                                                                       MEDLINE=93389738;
                                                                                                                                                                                                                                         SPECIES-Chicken
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                        terminals
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of the SNAP-25
(MAR-2000) to
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109:3039-3052(1989).
                                                                                                                                                           233:
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Mullahy S.J.,
naratne P.H.,
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RESULT
RRPP_HF
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Best Local
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P14156;
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01-JAN-1990
28-FEB-2003
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entities requires a
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Viruses;
                      Human respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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"Differential subcellular localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96346613;
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PTM: PALMITOYLATED.

SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.

SIMILARITY: Contains 2 t-SNARE coiled-coil homology
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Event-Alternative splicing; Named isc
Comment-Isoforms differ by the usag
homologous exons (5a and 5b) which
and differ only in 9 positions out
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A1023913; CAC34534 1; -...
AF240770; AAF64477, 1; -...
BC018249; AAA1121 -...
M2012; AAA61741.1; -...
BC018249; AAH18249, 1; -...
M57957; AAA49077.1; -...
AB003991; BAA20151, 1; -...
AB003991; BAA20151, 1; -...
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AB003991; BAA20152, 1; -...
L09253; AAA49070.1; JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=SNAP-25a;
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L19760; AAC37545.1;
D21267; BAA22370.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
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hl F., Bark I.C.,
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Pred. No.
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    viruses; Mononegavirales;
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tion of SNAP-25a and SNAP-25b RNA
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SEQUENCE FROM N.A.
SEQUENCE—85033973; PubMed=654
MEDLINE—85033973; PubMed=654
Satake M., Elango N., Venkat
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J. Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human respiratory syncytial virus (strain A2). Viruses; SsRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus. NCBI_TaxID-11259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRPP_HRSVA
P03421;
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J. Gen. Virol. 66:1607-1612(1985).
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28-FEB-2003 (Rel.
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NCBI_TaxID-11250;
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                         SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no restr
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that subunit (EC 2.7.7.48) (Phosphoprotein
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MOD_RES 116
MOD_RES 117
MOD_RES 119
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MOD_RES 156
MOD_RES 161
SEQUENCE 241 A
                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                          use
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                              MEDIINE=88323192; PubMed=3414184;
Lopez J.A., Villanueva N., Melero J.A., Portela A.;
"Nucleotide sequence of the fusion and phosphoprotein genes
respiratory syncytial (RS) virus Long strain: evidence of su
genetic heterogeneity.";
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01-OCT-1989 (Rel.
28-FEB-2003 (Rel.
           Pfam;
                                   EMBL; M22644; AAA47415.1; PIR; S07428; RRNZPP.
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or send an email to license@isb-sib.ch)
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Navarro J., Lopez-Otin C., Villanueva
"Location of phosphorylated residues:
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[2]
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polymerase;
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(See http://www.isb-sib.ch/announce/
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human respiratory syncytial
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Nucleocapsid;
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RESULT 8
1431_ECHMU
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1431_ECHGR
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MOD_RES 116
MOD_RES 117
MOD_RES 119
MOD_RES 143
MOD_RES 156
MOD_RES 161
SEQUENCE 241 A/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090408;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
14-3-3 protein homolog 1.
                                                                                                                                                                      PRINTS; PR00305; 1433ZETA.

ProDom; PD000600; 14-3-3; 1.

SMART; SM00101; 144_3_3; 1.

PROSITE: PS00796; 1433_1; FALSE_NEG
PROSITE: PS00797; 1433_2; 1.
                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          *Siles-Lucas M., Nunes C.P., Zaha A.;

*Comparative analysis of the 14-3-3 gene and its expression Echinococcus granulosus and Echinococcus multilocularis metacestodes **;
 1431_ECHMU
                                                                                                                                                              Multigene family
                                                                                                                                                                                                                                                       EMBL; AF207904
HSSP; P29312;
                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                   Parasitology 122:281-287(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21182697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda; Cyclophyllidea; Taeniidae; Echinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Echinococcus granulosus.
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                                                                                                                                                                                                                                 Pfam; PF00244; 14-3-3;
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                                                                                                                                                                                                                                                                                                                                                   between
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                                                                              EANQRAT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EANQRATK
                                                          EANQKAT 161
                                                                                                                                                  244 AA;
                                                                                                       Conservative
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85.7%;
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75.0%;
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Pred. No.
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DCB2D3942973DD59
 PRT;
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10;
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                                                                                                                           1; Length 244;
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                               TÖR2_SCHPO STANDARD; PRT; 2337 AA.

Q9Y7K2; 094507;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Fast annota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000308; 14-3-3.
Pfam; PE00244; 14-3-3; 1.
PRINTS; PR00305; 14-32ETA.
PRODOM; PD000600; 14-3-3; 1.
SMART; SM00101; 14-3-3; 1.
PROSITE; PS00796; 14-3-1; 1.
PROSITE; PS00797; 14-33-1; 1.
PROSITE; PS00797; 14-33-2; 1.
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A. Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Barooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multigene
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q24902;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
14-3-3 protein homolog 1 (Emmal4-3-3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Echinococcus multilocularis.
Eukaryota; Metazoa; Platyhelminthes; Cestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
                                                                                                                                                                                                                    STRAIN=972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multilocularis
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                                                                                                                                                                                      MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U63643; AAC48315.2; -. HSSP; P29312; 1A37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Biochem. Parasitol. 91:281-293(1998).
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244 AA;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
C 2.7.1.137) (PI3-kinase)
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RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S.,
RA Taylor K., Taylor R.G., Tivey A.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltlens I., Vanstreels E., Rleger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fruchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Garler F., Zimmermann W., Wedler H., Wambutt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Domanguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RI "The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
 REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. (
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                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                           PROSITE; PS50077; HEAT_REPEAT; 1.
PROSITE; PS00915; PI3_4_KINASE_1; 1.
PROSITE; PS50290; PI3_4_KINASE_3; 1.
Transferase; Kinase; Cell cycle; Rep
                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 276:7027-7032(2001).
                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL049558; CAB
PIR; T39913; T40577
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL035216; CAA22805.1; EMBL; AL049558; CAB40167.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       starvation and other
                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                  InterPro; IPR003151; FAT.
InterPro; IPR003152; FATC.
InterPro; IPR000357; HEAT_repeat.
InterPro; IPR000403; PI3_PI4_kinase.
                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The fission yeast TOR homolog, tor1+, is required for the starvation and other stresses via a conserved serine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weisman R., Choder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21269225;
                                                                              REPEAT
                                                                                                                   REPEAT
                                                                                                                                 REPEAT
                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                         GeneDB_SPombe; SPBC216.07c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-phosphatidy1-1D-myo-inositol 3-phosphate.
SIMILARITY: BELONGS TO THE PI3/PI4-KINASES
SIMILARITY: Contains 15 HEAT repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                progression (By similarity).
CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol
                                                                                                                                                                                                                                                                            PF00250; FATC; 2.
PF00454; PI3_PI4_kinase;
                                                                                                                                                                                                                                                                                                                                                                      P42345; 1AUE
                                                                                                                                                                                                                                                                  SM00146; PI3Kc;
                                                                                        163
249
290
409
474
474
642
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-i- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) -

CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF.
                                                                                                                                                                                                                                                                                                                                                                   involved in chloroplast division.";
Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
-!- CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) =
                                                                                                                                                                                                                                                                                                                                                                                                                            Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M.,
Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., H
Inamura A., Yoshinaga K., Sugiura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae;
Chlorellaceae; Chlorella.
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                                                                                                                              InterPro; IPR002146; ATPsynt_B/B'sub.
Pfam; PF00430; ATP-synt_B; 1.
                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequence of the chloroplast genome green alga Chlorella vulgaris: the existence of genes po
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STRAIN-IAM C-27 /
                                                                                                                                                     EMBL; AB001684; BAA57857.1; -. PIR; T07210; T07210.
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P56296;
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19 38 POTENTIAL.
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Pred. No. 1
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07F64D4B2C3BCF34 CRC64;
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2 P76637; P78217; Q46914;

10 1.NOV-1997 (Rel. 35, Created)

115-SEP-2003 (Rel. 40, Last sequence update)

115-SEP-2003 (Rel. 42, Last annotation update)

E Glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD).

E Glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD).

E Glucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD).

E Scherichia coli 0157:H7.

Escherichia coli 0157:H7.

Escherichia coli 0157:H7.

Escherichia coli 0157:H7.

Escherichia coli 0157:H7.

C Enterobatteriaceae; Escherichia.
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01-JUN-1994
01-JUN-1994
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01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Synaptosomal-associated protein 25 (SNAP-25).
Torpedo marmorata (Marbled electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea; Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Risinger C., Blomqvist A.G., Lundell I., Lambertsson A., Wassel D., Pieribone V.A., Brodin L., Larhammar D.; "Evolutionary conservation of synaptosome-associated protein (SNAP-25) shown by Drosophila and Torpedo cDNA clones:"; J. Biol. Chem. 268:24408-24414(1993).

-i- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Torpediniformes;
NCBI_TaxID=7788;
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MEDLINE-94043281; PubMed-8226991;
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SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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U29581; AAB40437.1; AE000362; AAC75829. AE005507; AAG57900.

AAG57900.1; -.; AAG57900.1; -.

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STRAIN=0157:H7 / RIMD 0509952;

MEDLINB=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97349980; PubMed-9205837;
Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Ison Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mits Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivas Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                           "Evolution of enzymatic activities in the enclase superfamily: characterization of the (D)-glucarate/galactarate catabolic pathwin Escherichia coli.";
in Escherichia coli.";
Biochemistry 37:14369-14375(1998).
-i- FUNCTION: CATALYZES THE DEHYDRATION OF GLUCARATE TO 5-KETO-4-DEOXY-D-GLUCARATE (5-KDGLUC). ALSO ACTS ON L-IDARATE.
-i- CATALYTIC ACTIVITY: D-glucarate = 5-dehydro-4-deoxy-D-glucarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.
Apodeca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                         -!- PATHWAY: Glucarate catabolism; first step.
-!- SIMILARITY: BELONGS TO THE MANDELATE RACEMASE
-LACTONIZING ENZYME FAMILY. GLUCD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Construction of a contiguous 874-kb sequence of the Escherichia KI2 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features."; DNA Res. 4:91-113(1997).
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MEDLINE-21074935; PubMed-11206551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-14, AND CHARACTERIZATION
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Mitsuhashi N.,
moto H.,
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P14380;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Transposon TX1 hypothetical 82 kba protein (ORF 1).

Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Cranifata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; G910
PDB; 1EC7
PDB; 1EC8
PDB; 1EC9
PDB; 1EC9
PDB; 1JCT
ECOGene;
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                            PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; ZDF_C2HC; 1.
Hypothetical proteth: Transposable element.
SEQUENCE 775 AA; 82355 MW; B8C361AEC65DD85B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89384562; PubMede2550791;
Garrett J.E., Knutzon D.S., Carroll D.;
"Composite transposable elements in the Xenopus laevis genome.";
Mol. Cell. Biol. 9:3018-3027(1989).
                                                                                                                                                                                                                                                                                                                                                                         EMBL; M26915; AAA49975.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                    PIR; A32494; A32494.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                  InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyase;
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G91084; G91084.
; LEC7; 23-MAY-00.
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1EC9; 23-MAY-00.
1ECQ; 23-MAY-00.
1JCT; 05-SEP-01.
594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome; ET 0 0
                                                                                              Similarity
6; Conserv
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EANHRASK 601
                                            EANQRATK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EG13167; gudD.
; IPR001354; MR_MLE.
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445 AA;
                                                                                              Conservative
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49010 MW;
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75.0%;
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75.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB Pred. No. 32; 0; Mismatches
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                                                                                           Score 30; DB 1; Pred. No. 57; l; Mismatches
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                                                                                                                                             Length 775;
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RESULT 14

3385

YLF6

CAEEL

STANDARD;

162

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Q03598; 01-FEB-1994 01-FEB-1994

(Rel.

28, 28,

Created)
Last sequence

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SYV_VIBCH
ID SYV_Y
AC Q9KP7
DT 16-0C
DT
RESULT 15
YLF6_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002303; tRNA-synt_val.
Pfam; PF00133; tRNA-synt_l; 1.
PRINTS; PR00986; TRNASYNTHVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; E82068; E82068.
HSSP; P96142; 1GAX.
TIGR; VC2503; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
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Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=E1 Tor N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                Complete
                                                                                                                                                                                                                                                                                                                                                                                                                          Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00422; valS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE004320; AAF95645.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY:
+ L-valyl-tRNA(Val).
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16-0CT-2001 (Rel.
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                                                                                                                                                                                                                          Similarity
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558
557
108170
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75.0%;
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Last annotation update)
(EC 6.1.1.9) (Valine--tRNA ligase) (ValRS).
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                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       Protein biosynthesis; Ligase; ATP-binding
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Pred. No. 71;
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P (BY SIMILARITY).
D93471A33CF4F69C
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                                                                                                                                                                                                                                                 Length 953;
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Sellers P.,
White O.,
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Matches 5
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Nature 368:32-38(1994).
-i- SIMILARITY: STRONG, TO HUMAN CGI-126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., Shownkeen R.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.;
"2. 2 M b of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S28301; S28301.
WormPep; C40H1.6; CE00114.
Hypothetical protein.
SEQUENCE 162 AA; 18537 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-94150718; PubMed-7906398;
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z19154; CAA79557.1; -.
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Hypothetical protein C40H1.6 in chromosome III.
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                                                                                                                                                                                                     EANQRATK 8
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62.58;
                                  2003, 19:27:05
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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SEC9 protein - yea
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SNAP-25 protein
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ALIGNMENTS

R;Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C. Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coin A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Status: preliminary

A; Molecule type: mRNA A; Residues: 1-206 < CAT> C:Species: Gallus gallus (chicken)
C:Date: 30-Apr-1991 #sequence_revision
C:Accession: A37861

30-Apr-1991 #text_change 21-Jul-2000

synaptosomal-associated 25K protein - chicken

```
RESULT 2
167823
nerve terminal protein - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 29-May-1998 #sequence_revision 29
C; Accession: 167823
R; Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
                                                          A;Title: Human cDNA clones encoding two different isoforms A;Reference number: I53735; MUID:94156217; PMID:8112622 A;Accession: I67823
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                A; Molecule type: mRNA
A; Residues: 1-206 < RES>
                                               A; Status: preliminary; translated
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A;Cross-references: GB:L19761; NID:g307427; PIDN:AAC37546.1; PID:g307428
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206; Conserv
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                                                 from GB/EMBL/DDBJ
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nerve terminal protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision
C:Accession: IS3735
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billi J. Cell Biol. 109, 3039-3052, 1989
A:Title: The identification of a novel synaptosomal-associated A:Reference number: A33623; MUID:90078337; PMID:2592413
A:Accession: A33623
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synaptosomal-associated 25K protein - m
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision
C;Accession: A33623
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A33623
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A;Gene: GDB:SNAP
A;Cross-references: GDB:355671;
A;Map position: 20p11.2-20p11.2
 A; Title: Human cDNA
A; Reference number:
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A; Residues: 1-206 <OYL>
A; Cross-references: GB: M22012;
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 153735;
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encoding two different isoforms; MUID:94156217; PMID:8112622
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Pred. No. 4
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Pred. No. 4.6e-63;
Mismatches 0;
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1.6e-63;
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RESULT 6 S38309 SNAP-25 |

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C;Accession: 150480

R;Risinger, C.; Larhammar, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993

A;Title: Multiple loci for synapse protein SNAP-25 in the synapse number: A49632; MUID: 94068448; PMID: 8248151

A;Accession: I50480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: I53735
A;Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: GB:L19760; NII
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C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision
C;Accession: I50480
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A;Cross-references: GDB:355671;
A;Map position: 20p11.2-20p11.2
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A; Gene: SNA
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A; Residues: 1-204 <RIS>
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                                                              VDEREQMAISGGFIRRYTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR
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93.2%;
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Pred. No. 3.8e-58;
6; Mismatches 6;
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C;Species: Gallus gallus (chicken)
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-199
C;Accession: S38309
R;Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A;Title: Structure of the chicken gene for SNAP-25 reveals duplicated exon A;Reference number: S38308; MUID:93389738; PMID:8377193
A;Accession: S38309
A;Status: preliminary; translation not shown
A;Residues: 1-249 cBAR>
A;Residues: 1-249 cBAR>
A;Cross-references: EMBL:L09250
C;Genetics:
A;Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3
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Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993

A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid gold A;Reference number: A49632; MUID:94068448; PMID:8248151

A;Accession: I50481

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-203 <RIS>
A;Cross-references: GB:L22976; NID:9349430; PIDN:AAA16538.1; PID:9349431
C;GenetLcs:
A;Genes: SNAP-25
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C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50481
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Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 178
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89.3%;
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100.0%; Pred. No. 1e-55;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                     Score 933.5; DB 2; Pred. No. 1.9e-55;
                                                                                                                                                                                                                                                                                                    Mismatches
203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNAP-25 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_chang
C;Accession: S38308
R;Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A;Title: Structure of the chicken gene for SNAP-25 reveals dup
A;Reference number: S38308; MUID:93389738; PMID:8377193
A;Accession: S38308
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <BAR>
A;Residues: 1-249 <BAR>
                                                                                                                                                                                                                                                                                                                                                                      synapse protein - marbled electric ray

(;Species: Torpedo marmorata (marbled electric ray)

C;Date: 13-Sep-196 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Accession: I50552

R;Risinger, C; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone,

J. Biol. Chem. 268, 24408-24414, 1993

A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25)

A;Recession: I50552

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: GB:L22020; NID:g431296; PIDN:AAA49284.1; PID:g431297
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150552
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C;Genetics:
A;Introns: 24/3; 38/3; 55/1; 94
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Best Local S
Matches 164
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Best Local
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                                                   123 EREQMAISGGFIRRYTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIM
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                                                                                                                                                                                                                                             164;
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                                                                                                                                                                                                                                         h 79.9%; Score 837.5; DB 2;
Similarity 81.6%; Pred. No. 4.8e-49;
64; Conservative 16; Mismatches 18;
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                                                                                                             QINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSD---AYKKAWGNNQDGVVASQPARVVD 122
                 DREQMAMSGGYIRRITDDARENEMEENLDQVGSIIGNLRHMALDMSNEIGSQNAQIDRIV
                                                                                          QINKDMKEAEKNLSDLGKCCGLCSCPCNKLKNFEAGGAYKKVWGNNQDGVVASQPARVMD
                                                                                                                                                                DPRSEQEEMQRCADQITDESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMD
                                                                                                                                                                                    DMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMD
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95.1%;
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Pred. No. 8.6e-53;
5; Mismatches 4
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                                                                                                                                                                                                                                                                            Length 210;
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Gaps

69

189 182 129 0;

Gaps

180

120 120 60 exons

encoding

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vesicle-membrane fusion protein SNAP-23A - human C:Species: Homo sapiens (man) C:Date: 02-May-1997 #sequence_revision 18-Jul-1997 C:Accession: JC5296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10

JCS512

SNARE protein 23 - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C; Accession: JC5512
R; Araki, S; Tamori, Y; Kawanishi, M; Shinoda, H.; Masugi, J.; Mori, H.; Naccession: Biophys. Res. Commun, 234, 257-262, 1997
A; Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.
A; Reference number: JC5512; MUID:97312558; PMID:9168999
A; Accession: JC5512
                 δõ
                                                                                                                                                                                                                                                                                                                                              C;Accession: JC5296
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5296
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A;Residues: 1-211 <MOL>
A;Residues: 1-211 <MOL>
A;Cross-references: GB:Y09567; NID:g1924941; PIDN:CAA70760.1; PID:e290695; PID:g1924942
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
JC5296
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A; Residues: 1-210 <ARA>
A; Cross-references: DDB
C; Comment: This protein
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                 EQM---
                                                RETEKTLTELNKCCGLCVCPCNRTKNFESGKAYKTTWGDGGENSPCNVVSKQPGPVTNGQ
                                                                       KEAEKNLTDLGKFCGLCVCPCNKLK---SSDAYKKAWG---
                                                                                                                                    EEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKDM 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEKADSNKTRIDEANQRATKMLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEAEKNLTDLGKFCGLCVCPCNKLKSSDA---YKKAWG----NNQDGVVASQPARVVDER 124
                                                                                                                    EEIQQRAHQITDESLESTRRILGLAIESQDAGIKTITMLDEQKEQLNRIEEGLDQINKDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQM --- AISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRI 181
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-AISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR
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                                                                                                                                                                                                        58.2%;
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Pred. No. 2.7e-36;
                                                                                                                                                                                                        Score 609.5; DB 2; Pred. No. 7.4e-34;
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C;Accession: JC5297

C;Accession: JC5297
                                                                                                                                                                                                                                                                                                                                                             vesicle-membrane fusion protein SNAP-23B - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997
                                                                                                                                                             A;Cross-references: GB:Y09568; NID:g1924943; PIDN:CAA70761.1; PID:e290774; PID:g19249
A;Experimental source: neutrophils
                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-158 < MOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y22F5A.3 - Caenori
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T26553
                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown; translation not shown
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A; Introns: 51/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-234 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL021479; PIDN:CAA16322.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data A; Reference number: Z20231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Gardner, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
                                                                                                                                            This protein is involved in regulating exocytosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                        Similarity
DKAQSNEVRVESANKRAKNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADMRNELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDSSMGPQGGYITKITNDAREDEMDENVQQVSTMVGNLRNMAIDMSTEVSNQNRQLDRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTINQDMKEAEDHLKGMEKCCGLCVLPWNKTDDFEKTEFAKAWKKDDDGGVISDQPRITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQINKDMKEAEKNLTDLGKFCGLCVCPCNKLKSSD--AYKKAWGNNQDGVVASQPARVVD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADMSDELKGLNVGIDEKTIESLESTRRMLALCEESKEAGIKTLVMLDDQGEQLERCEGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKADSNKTRIDEANQRATKML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMEKADSNKTRIDEANQRATKMLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITDKADTNRDRIDIANARAKKLIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQQPTTGAASGGYIKRITNDAREDEMEENLTQVGSILGNLKDMALNIGNEIDAQNPQIKR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82/1; 165/2; 213/3
                                                                         Conservative
                                                                                        48.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library,
                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                  SNAP-23B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
                                                                       Score 512; DB
Pred. No. 1.7e
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 541; DB 2
Pred. No. 3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998
                                                                   DB 2; 1
1.7e-27;
hes 26;
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                                                                                                                                                                                                                                                                                                                                                               #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPDB:GN00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 234
                                                                                                       Length 158
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                       42;
                                                                                                                                              human
                                                                                                                                                                                                                                                                                         fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                              neutrophils,
                                                                                                                                                                                                                                                                                         protein
                                   71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                           SNAP-2
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C;Accession: A86272

C;Accession: A86272

C;Accession: A86272

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.E.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                   submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid K02D10.
A;Reference number: S44605
A;Accession: S44837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein F16A14.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
A86272
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: F16A14.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-263 <S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE005172; NID:g8778388; PIDN:AAF79396.1; GSPDB:GN00141
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                   111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-263 <STO>
                                                                                                                                                                                                                                                                                                                                                                        QPALDQPTNALQKVEQ------
                                                                                                                                                                                                                                                                                                                                                                                                  GVVASQPARVVDEREQMAISGGFIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELEKYAVYKAETTKGVNNCLKIAEDIRSDGARTLEMLHQQGEQINRTHEMAVDMDKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RETEKTLTELNKCCGLCVCPCNS---
                                                                                                                                                                                                                                                                                                                               IDTONROIDRIMEKADSNKTRIDEANORATKML
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRGEKLLNNLGGMFSKPWKPKKTKNITGPMITPDKPSKKSENHKEEREKLGLGAKGRSSS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEAEKNLTDLG------KFCGLCVCPCNKLKSSDAYKK-----AWGNNQD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKDM 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFIRRYTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDIANARAKKLIDS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDEANQRATKMLGS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARVVDEREQMAISG
                                                                                                                                                                                                                                                                                        IDKONKALDHLGDDVDELNSRVQGANQRARHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ITNDAREDEMEENLTQVGSILGNLKDMALNIGNEIDAQNPQIKRITDKADTNRDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.3%; Score 255; DB 2; I
29.1%; Pred. No. 3.7e-10;
tive 39; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                        -----EKAKQDDGLSDLSDILGDLKSMAVDMGSE 228
                                                                                                                                                                                                                                                                                          261
                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
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Qy
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C;Genetics:
A;Introns: 260/2; 318/1; 506/1; 528/1; 639/3; 746/3
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A; Residues: 1-786 < AND>
                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                           Query Match
Best Local
 717
                                     169
                                                                                                            129
                                                                                                                                              603
                                                                                                                                                                                                                   543 DEADYYEREIEKTLQESLDSTERSRRHLENSEKIGTSTAQQLLEQREKLENTEKNLDEIH
                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                                   9 NELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQIN 68
                                                                                                                                                                                                                                                                                                           Similarity
                  NEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
                                                                                                              ISGG---
                                                                                                                                            RTTQMTQRNLNSLKSFFG-----GMFKNKFTKKPQEPTETPTVPQSKSASRLSETATNL
                                                                                                                                                                                KDMKEAEKNLTDLGKFCGLCVCPCNKLKSSDAYKKAWGNNQDGVVASQPARVVDEREQMA 128
KEVDSQNEMLDRIQYKAERNDGIVRDQDKQMQKILGTG
                                                                       SSGGGSATFSGPSGQRTLTESSRSAIKGTRWEAMDNQIDENLDMMSANLRNLQRLGADLG
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                         22.8%; Score 239; DB 2; 28.0%; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                      43; Mismatches
                                                                                                        --FIRRVTNDARENEMDENLEQVSGIIGNLRHMALDMG 168
                                                                                                                                                                                                                                                                                                                          Length 786;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                              , 656
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Search completed: September 16, 2003, 19:30:47 Job time: 54.5065 secs

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